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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:03:31 ; Search time 73.16 Seconds
(without alignments)
215,589 Million cell updates/sec

Title: us-09-781-077-2
Perfect score: 760
Sequence: 1 MARYMLLLAVVLTGELW.....GLSSCKCKGCKSKBSISLIC 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
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10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match Length | ID | Description |
|------------|-------------|--------------|-----|-------------|
| 1 | 760 | 100.0 | 142 | 22 AAG78114 |
| 2 | 148 | 19.5 | 135 | 21 AAY95771 |
| 3 | 147 | 19.3 | 135 | 19 AAW37926 |
| 4 | 126.5 | 16.6 | 135 | 19 AAW37925 |
| 5 | 126.5 | 16.6 | 135 | 20 AAY01961 |
| 6 | 126.5 | 16.6 | 135 | 21 AAB00173 |
| 7 | 126.5 | 16.6 | 135 | 21 AAB24391 |
| 8 | 126.5 | 16.6 | 135 | 21 AAY95770 |
| 9 | 126.5 | 16.6 | 135 | 21 AA183228 |
| 10 | 126.5 | 16.6 | 135 | 22 AA24033 |
| 11 | 126.5 | 16.6 | 135 | 22 AAU12309 |

| | | | | | |
|----|-------|------|-----|-------------|---------------------|
| 12 | 126.5 | 16.6 | 135 | 22 AAB20110 | Human immunostimul |
| 13 | 126.5 | 16.6 | 135 | 22 AAB53072 | Human angiogenesis |
| 14 | 111.5 | 14.7 | 185 | 5 AAP40108 | Sequence of human |
| 15 | 109.5 | 14.4 | 185 | 10 AAP94621 | Amino acid sequenc |
| 16 | 108.5 | 14.3 | 182 | 5 AAP40156 | Sequence of porcine |
| 17 | 107.5 | 14.1 | 162 | 11 AAR07987 | H2 prorelaxin gene |
| 18 | 106.5 | 14.0 | 182 | 4 AAP30392 | Sequence of porcine |
| 19 | 102.5 | 13.5 | 164 | 11 AAR07988 | H2 prorelaxin dedu |
| 20 | 98.5 | 13.0 | 185 | 5 AAP40154 | Sequence of human |
| 21 | 94.5 | 13.0 | 185 | 5 AAP40155 | Sequence of human |
| 22 | 94.5 | 12.4 | 185 | 5 AAP94622 | Amino acid sequenc |
| 23 | 92.5 | 12.2 | 40 | 17 AAP96006 | Asymmetry sequence |
| 24 | 92 | 12.1 | 30 | 20 AAY01963 | Insulin-like pepti |
| 25 | 92 | 12.1 | 31 | 21 AAY95773 | Human zins3 B chal |
| 26 | 89.5 | 11.8 | 150 | 16 AAR64904 | Prorelaxin fragme |
| 27 | 88.5 | 11.6 | 134 | 21 AAY71544 | Drosophila melanog |
| 28 | 88.5 | 11.6 | 134 | 21 AAY99807 | Drosophila dmsl i |
| 29 | 88.5 | 11.6 | 134 | 22 ABB62638 | Drosophila melanog |
| 30 | 88.5 | 11.6 | 188 | 19 AAW47547 | Rat zins2 testis-s |
| 31 | 87 | 11.4 | 220 | 22 AAU02911 | Angiotensin conver |
| 32 | 86.5 | 11.4 | 110 | 22 AAB84818 | Protein. Unidenti |
| 33 | 86.5 | 11.4 | 178 | 14 AAR31958 | Squamous cell spec |
| 34 | 84.5 | 11.1 | 110 | 2 AAP10042 | Sequence encoded b |
| 35 | 84.5 | 11.1 | 110 | 2 AAP10053 | Sequence of prepro |
| 36 | 84.5 | 11.1 | 110 | 5 AAP40309 | Human preproinsuli |
| 37 | 84.5 | 11.1 | 110 | 20 AAY06608 | Human preproinsuli |
| 38 | 84.5 | 11.1 | 110 | 21 AAB26765 | Human insulin. Ho |
| 39 | 84.5 | 11.1 | 110 | 21 AAB06144 | Human Insulin used |
| 40 | 84.5 | 11.1 | 110 | 21 AAY70366 | Human proinsulin n |
| 41 | 84.5 | 11.1 | 110 | 22 AAY44367 | Human proinsulin |
| 42 | 84.5 | 11.1 | 110 | 22 AAG65877 | Human pre-proinsul |
| 43 | 84.5 | 11.1 | 110 | 22 ABE10337 | Secretory cell lin |
| 44 | 84.5 | 11.1 | 110 | 22 AAB35424 | Human insulin prec |
| 45 | 82.5 | 10.9 | 110 | 22 AAB48847 | |

ALIGNMENTS

| | |
|----------|---------------------------------------------------------------------------|
| RESULT | 1 |
| AAG78114 | |
| ID | AAG78114 standard; Protein; 142 AA. |
| XX | |
| AC | AAG78114; |
| XX | |
| DT | 21-NOV-2001 (first entry) |
| XX | |
| DE | Human insulin homologue polypeptide zins4. |
| XX | |
| KW | Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; |
| KW | antifertility; vasotropic; reproductive disorder; prostate disorder; |
| KW | heart disorder; kidney disorder; gonadal development; pregnancy; |
| KW | pubertal change; menopause; ovarian cancer; testicular cancer; ovulation; |
| KW | polycystic ovarian syndrome; contractile tissue; cardiovascular disease; |
| KW | blood control; impotence; myocyte; endothelial cell; osteoblast; |
| KW | birth pressure; muscle tension; osmotic balance; gene therapy. |
| OS | Homo sapiens. |
| XX | |
| PH | Key |
| FT | Location/Qualifiers |
| FT | Peptide |
| FT | 1..25 |
| FT | /label= signal_peptide |
| FT | 26..142 |
| FT | /label= mature_protein |
| FT | /note= "zins4, Claimed in claim 4" |
| FT | 26..52 |
| FT | /label= B_chain |
| FT | /note= "Claimed in claim 1" |
| FT | 34..47 |
| FT | /label= B_chain_consensus_sequence_region |
| FT | /note= "Given in SEQ ID NO 3" |
| FT | 37..41 |
| FT | /label= B_chain_conserved_motif |

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FT FT /note= "Given in SEQ ID NO 5"
FT FT 53..54
FT FT /label= C_peptide
FT FT 55..118
FT FT /label= A_chain
FT FT 55..114
FT FT /note= "Claimed in claim 3"
FT FT 115..118
FT FT /note= "Cleavage site at the junction of the C peptide
FT FT and the A chain with a conserved RXXR motif"
FT FT 119..142
FT FT /label= A_chain
FT FT /note= "Claimed in claim 2"
FT FT 128..142
FT FT /label= A_chain_consensus_sequence_region
FT FT /note= "Given in SEQ ID NO 4"
XX WO200168862-A1.
XX 20-SEP-2001.
XX 09-FEB-2001; 2001WO-US04199.
XX 10-MAR-2000; 2000US-0523346.
XX (ZYMO) ZYMOGENETICS INC.
XX Holloway JL, Lok S, Jaspers SR;
XX WPI: 2001-582454/65.
XX N-PSDB; AAH79088.
XX New insulin homologue polypeptide having homology to relaxin family,
XX designated zins4 and zins4 polynucleotide, useful for diagnosing,
XX preventing, treating reproductive, prostate, heart and kidney disorders
XX
XX Claim 6; Page 72-73; 79pp; English.
XX The invention relates to an isolated insulin homologue zins4 having
XX homology to the relaxin family. The zins4 gene, located on chromosome
XX 19p13.11, encodes a 142 amino acid protein, where the zins4 polypeptide
XX comprises a B chain and A chain comprising amino acid residues 26-52 and
XX 119-142 respectively, joined by inter- and intra-chain disulfide bonds.
XX Zins4 has cytostatic, antifertility and vasotropic activity. Zins4
XX proteins are useful in applications for enhancing fertilisation during
XX assisted reproduction in humans and animals and in therapies for treating
XX reproductive disorders. Zins4 protein is useful in treating reproductive,
XX prostate, heart or kidney disorders and to identify cells, tissues or
XX cell lines which respond to the zins4-stimulated pathway and to identify
XX inhibitors of its activity. Zins4 polypeptides and modulators of the
XX polypeptide are useful in treating disorders associated with gonadal
XX development, pregnancy, pubertal changes, menopause, ovarian cancer,
XX prostate, testicular cancer, fertility, ovarian function, ovulation,
XX polycystic ovarian syndrome and other reproductive functions including
XX pathological conditions in ovary. Detection of zins4 polypeptides in the
XX serum or tissue biopsy of a patient is useful for diagnosing ovarian
XX cancer. The molecules are also useful for treating dysfunction associated
XX with contractile tissues or to suppress or enhance contractility in vivo,
XX treating cardiovascular disease, infertility, in vitro fertilization,
XX birth control, treating impotence or other male reproductive dysfunction,
XX inducing birth, for promoting growth, differentiation, development and/or
XX maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in
XX culture and in the study of the ovarian cycle, reproductive function,
XX ovarian cell-cell interactions and fertilisation. The polypeptide is also
XX useful as a modulator of blood pressure, muscle tension and osmotic
XX balance. The zins4 polynucleotide is useful in gene therapy.
XX
XX Sequence 142 AA;

Query Match 100.0%; Score 760; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 1e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARYMLLLAVVLTGELWFGAARAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||| 60
1 maryml|||llavv||tgelwpgaaaraapgyvrlcgrrefiraviftcgswrrsdilah 60
QY 61 EAMGTFPDADADESLAGELDEAMSGSEWLATKSPQAFYRGPRPSWOGTGVLRGSRDV 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||| 120
61 eamgdtfpdadadedslageldeamsgswwlaltkspqafyrgprpswogtgvlgrrsdv 120
QY 121 LAGLSSSCCKGCKSEKSEISSIC 142
DB |||||||||||||||||||||||||||||||||||||||||||||||||||| 142
121 laglssscckgckskseissic 142
RESULT 2
AAAY95771
ID AAY95771 standard; Protein; 135 AA.
XX AAY95771;
XX 07-NOV-2000 (first entry)
XX Mouse insulin family homologue zins3.
XX zins3; insulin; relaxin; mouse; NIDDM;
XX non-insulin dependent diabetes mellitus; diagnosis.
XX Mus musculus.
XX WO200047776-A2.
XX 17-AUG-2000.
XX 10-FEB-2000; 2000WO-US03515.
XX 12-FEB-1999; 99US-0198248.
XX 12-FEB-1999; 99US-0250125.
XX (ZYMO) ZYMOGENETICS INC.
XX Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
XX WPI: 2000-558220/51.
XX N-PSDB; AAA50153.
XX Identifying mutations in human chromosome 1p31, preferably a zins3 gene
XX mutation, comprises using an insulin/relaxin family member (designated
XX zins3), useful for diagnosing non-insulin dependent diabetes -
XX
XX Example 4; Page 46-47; 51pp; English.
XX The present sequence is that of a murine paralog (see AAY95771) of
XX human zins3 (see AAY95770), a novel member of the insulin/relaxin
XX family member that maps to a region of human chromosome 1 associated
XX with non-insulin dependent diabetes mellitus (NIDDM). The sequence
XX was deduced from an isolated cDNA clone (see AAA50153). Northern
XX blots of embryo tissue indicated that mouse zins3 is expressed in
XX a developmentally regulated fashion. zins3 polynucleotides and
XX polypeptides can be used to diagnose disorders associated with
XX abnormal expression of zins3, and to identify polymorphisms that
XX result from mutations in the human zins3 gene. The invention
XX provides methods for identifying abnormalities in expression that
XX are a factor in causing, or predisposing, a person to some defect
XX in glucose metabolism, such as NIDDM.
XX
XX Sequence 135 AA;

Query Match 19.5%; Score 148; DB 21; Length 135;
Best Local Similarity 29.9%; Pred. No. 2.8e-08;
Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

QY 1 MARYMLLLAVVLTGELWFGAARAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60

Db 6 lalflilvilav-----vevrsr-qtkicgldyrtviycassrwrh----- 49
 QY 61 EAMGDFPPADADESLAGELDEAMGSSEWL-----ALTKSQAFYRGPSWQ 108
 Db 50 --legfhfsqgaetnylqlldrbpskktlehsplktdlsgqelvdqapkeg--lwe 105
 QY 109 GTPGVLRGSRDVLAGLSSCKCKWCSKSEISLCL 142
 Db 106 lkkhsvvrrd----lqalcrcgcmkclstic 135

RESULT 3
 AAW37926
 ID AAW37926 standard; Protein; 135 AA.
 AC AAW37926;
 XX
 DT 01-SEP-1998 (first entry)
 DE Mouse Zins3 protein.
 KW Insulin homologue; identification; isolation; Zins3 receptor;
 KW treatment; disease; pre-eclampsia; premature labour; Human.
 OS Mus sp.
 FH Key
 FT Peptide
 FT 23..48
 FT /note= "B chain"
 FT 49..115
 FT /note= "C-peptide"
 FT 116..135
 FT /note= "A chain"
 PN W09816635-A1.
 XX
 XX 23-APR-1998.
 XX
 XX 15-OCT-1997; 97WO-US18593.
 XX
 XX 15-OCT-1996; 96US-0028177.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
 XX WPI; 1998-251285/22.
 XX N-PSDB; AAV29153.
 XX
 XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
 XX treat pre-eclampsia, premature labour and Crohn's disease
 XX
 XX Claim 9; Page 67; 81pp; English.
 XX
 XX The Zins3 protein is an insulin homologue protein. Polynucleotide
 XX molecules taken from its gene can be introduced into a cultured cell
 XX using an expression vector. The cell will express an insulin homologue
 XX polypeptide encoded by the polynucleotide. The polypeptides can also be
 XX expressed by introducing the polynucleotides into the germline of a
 XX nonhuman animal. The polypeptides can be used to identify and isolate
 XX receptors for zins3. Antibodies and antagonists of the polypeptides can
 XX be used for treating disease associated with extracellular matrix and
 XX vessels. The antibodies may also be used in the diagnosis of diseases
 XX associated with the polypeptide, such as reproductive disorders
 XX placental and colon pathology. Antagonists against the polypeptide may
 XX also be used to treat diseases such as pre-eclampsia, premature labour, and
 XX Crohn's disease.
 XX
 XX Sequence 135 AA;

Query Match 19.3%; Score 147; DB 19; Length 135;
 Best Local Similarity 29.9%; Pred. No. 3.6e-08;
 Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;
 QY 1 MARYMLLLLVWVLTGELWPCAEARAAPYGVRLCGREFTRAVITCGGSRWRRSDILAH 60
 Db 6 lalflilvilav-----vevrsr-qtkicgldyrtviycassrwrh----- 49
 QY 61 EAMGDFPPADADESLAGELDEAMGSSEWL-----ALTKSQAFYRGPSWQ 108
 Db 50 --legfhfsqgaetnylqlldrbpskktlehsplktdlsgqelvdqapkeg--lwe 105
 QY 109 GTPGVLRGSRDVLAGLSSCKCKWCSKSEISLCL 142
 Db 106 lkkhsvvrrd----lqalcrcgcmkclstic 135

RESULT 4
 AAW37925
 ID AAW37925 standard; Protein; 135 AA.
 AC AAW37925;
 XX
 DT 01-SEP-1998 (first entry)
 DE Human Zins3 protein.
 KW Insulin homologue; identification; isolation; Zins3 receptor;
 KW treatment; disease; pre-eclampsia; premature labour; Human.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT 23..48
 FT /note= "B chain"
 FT 49..114
 FT /note= "C-peptide"
 FT 115..135
 FT /note= "A chain"
 PN W09816635-A1.
 XX
 XX 23-APR-1998.
 XX
 XX 15-OCT-1997; 97WO-US18593.
 XX
 XX 15-OCT-1996; 96US-0028177.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
 XX WPI; 1998-251285/22.
 XX N-PSDB; AAV29150.
 XX
 XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
 XX treat pre-eclampsia, premature labour and Crohn's disease
 XX
 XX Claim 2; Page 64-65; 81pp; English.
 XX
 XX The Zins3 protein is an insulin homologue protein. Polynucleotide
 XX molecules taken from its gene can be introduced into a cultured cell
 XX using an expression vector. The cell will express an insulin homologue
 XX polypeptide encoded by the polynucleotide. The polypeptides can also be
 XX expressed by introducing the polynucleotides into the germline of a
 XX nonhuman animal. The polypeptides can be used to identify and isolate
 XX receptors for zins3. Antibodies and antagonists of the polypeptides can
 XX be used for treating disease associated with extracellular matrix and
 XX vessels. The antibodies may also be used in the diagnosis of diseases
 XX associated with the polypeptide, such as reproductive disorders
 XX placental and colon pathology. Antagonists against the polypeptide may
 XX also be used to treat diseases such as pre-eclampsia, premature labour, and

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CC      Crohn's disease.
XX      Sequence      135 AA;
SQ
Query Match          16.6%; Score 126.5; DB 19; Length 135;
Best Local Similarity 30.8%; Pred. No. 6.1e-06;
Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

QY      32 VPLCGRETRAVIFTCGGRWRR-----SDILAH-----EAMGDTEFDA 70
        |||||.:|||:|.:|||||
Db       26 vrlcgleylrtyivycassrrrhleglpqagaetgnsfqlphkrefseepagnlpkv 85
        |||||.:|||:|.:|||||

QY      71 DAD-EDSLAGELDEAMGSEWLATKSPQAFYRGPSWQGTGVLGRSRDVLGLSSCC 129
        |||||.:|||:|.:|||||
Db       86 dasgedrlwg-----gqmpteeelwskkhvmsrqd-----lqtlec 122
        |||||.:|||:|.:|||||

QY      130 KWGCSKEISLLC 142
        |||||.:|||:|.:|||||
Db       123 tdgcsmdisalc 135
        |||||.:|||:|.:|||||

RESULT      5
RAY01961
ID      RAY01961 standard; Protein; 135 AA.
XX
AC      RAY01961;
XX
DT      01-JUL-1999 (first entry)
XX
DE      pro-insulin-like peptide (pro-ILP).
XX
KW      Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
KW      A chain; B chain; C chain; neurophysiological function;
KW      fluid homeostasis; electrolyte homeostasis; cardiovascular function;
KW      blood pressure; somatic; cardiac ionotropic activity;
KW      cardiac chronotropic activity; collagen deposition.
XX
OS      Homo sapiens.
XX
WO9915664-A1.
XX
PD      01-APR-1999.
XX
PF      28-AUG-1998; 98WO-US17888.
XX
PR      24-SEP-1997; 97US-0059836.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Gurney A.;
XX
WPT; 1999-254713/21.
DR      N-P5DB; AXA35204.
XX
XX      Colon and uterus expressed insulin-like polypeptide, useful in the
PT      treatment of disorders related to neurophysiological function
XX
XX      Claim 5; Fig 6B; 75pp; English.
XX
XX      The present sequence represents an insulin-like polypeptide (pro-ILP).
CC      The protein is expressed in the colon and uterus, and is a member
CC      of the insulin/IGF family. The immature pro-ILP comprises a 135 amino
CC      acid sequence, which is processed into the mature form which comprises
CC      an A chain and a B chain linked by disulfide bonds. The C-peptide of
CC      pro-ILP exists as a separate peptide after processing of pro-ILP. The
CC      ILP protein is useful in treatment of disorders related to
CC      neurophysiological function affecting fluid homeostasis, electrolyte
CC      homeostasis, cardiovascular function, blood pressure, somatic or cardiac
CC      ionotropic activity, cardiac chronotropic activity and collagen
CC      deposition. The methods can be used for diagnosing a physiologic or
CC      pathologic condition of the uterus, colon or other ILP-expressing cell
CC      or tissue and for diagnosis and screening of modulators and therapeutics.
CC

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Composition for inhibiting neoplastic cell growth and treating cancers

PT of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
 XX PRO538, PRO172 or PRO182 polypeptide or their agonist
 PS Claim 14; Figure 10; 122pp; English.

CC Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
 CC polypeptide or their agonists, mixed with a carrier is useful for
 CC inhibiting neoplastic growth and treating tumors such as cancers of
 CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
 CC central nervous system, melanoma and leukaemia.

XX Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 21; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;
 QY 32 VRLCGREFIRAVITCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 DB 26 VRLCGLEYIRTVIYICASSRWRRHLEGPQAQAGTNSFQLPHKREFSEENPAQNPVKV 85
 QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGPRSWQGTGVLGRSDVLAGLSSCC 129
 DB 86 dasgedrlwg-----gqmpteelwskkhsvmsrkd-----lqtlcc 122
 QY 130 KWGCKSEISSLC 142
 DB 123 tdgcsmtldlsalc 135

RESULT 10

AAU24033

ID AAU24033 standard; Protein; 135 AA.

AC AAU24033;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1558.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX N-PSDB; AAH98692.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use

XX Claim 20; Page 1068-1069; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.

XX Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 22; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;
 QY 32 VRLCGREFIRAVITCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 DB 26 VRLCGLEYIRTVIYICASSRWRRHLEGPQAQAGTNSFQLPHKREFSEENPAQNPVKV 85
 QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGPRSWQGTGVLGRSDVLAGLSSCC 129
 DB 86 dasgedrlwg-----gqmpteelwskkhsvmsrkd-----lqtlcc 122
 QY 130 KWGCKSEISSLC 142
 DB 123 tdgcsmtldlsalc 135

RESULT 11

AAU12309

ID AAU12309 standard; Protein; 135 AA.

AC AAU12309;

XX 24-OCT-2001 (first entry)

XX Human PRO182 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

XX adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX 09-DEC-1999; 99US-0170262.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 30-DEC-1999; 99WO-US31243.

XX 06-JAN-2000; 2000WO-US00277.

XX 11-FEB-2000; 2000WO-US00376.

XX 18-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04342.

XX 24-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 01-MAR-2000; 2000WO-US05004.

XX 20-MAR-2000; 2000WO-US05601.

XX 21-MAR-2000; 2000WO-US07377.

XX 30-MAR-2000; 2000WO-US07532.

XX 30-MAR-2000; 2000WO-US08439.

PRO182; UNQ156; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antiallergic; immunostimulant.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..18 /label= Signal_peptide
Protein 19..135 /label= Mature_protein
Modified-site 107..111 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
Modified-site 3..9 /note= "N-myristoylation site"
Modified-site 52..58 /note= "N-myristoylation site"
Modified-site 96..102 /note= "N-myristoylation site"
Modified-site 125..131 /note= "N-myristoylation site"
Peptide 121..136 /note= "insulin family signature"

WO200105972-A1.
25-JAN-2001.
15-MAR-2000; 2000WO-US06884.
20-JUL-1999; 99US-0144758.
(GETH) GENENTECH INC.
Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK; Wood WI;
WPI; 2001-103149/11.
N-PSDB; AAF30052.
New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
Claim 20; Fig 6; 127pp; English.
The present sequence is that of PRO182 (UNQ156), a novel human immunomodulator protein encoded by cDNA (see AAF30052) isolated from a uterine cDNA library. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO182. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising the PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering the PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated

17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.
(GETH) GENENTECH INC.
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2001-408281/43.
N-PSDB; AAS21381.
Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -
Claim 12; Fig 276; 813pp; English.
AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Sequence 135 AA;
Query Match 16.6%; Score 126.5; DB 22; Length 135;
Best Local Similarity 30.8%; Pred. No. 6.1e-06;
Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;
QY 32 VRLCGREFIRAVITGGSRRR-----SDILAH-----RAMGDTTPDA 70
Db 26 vrlcgleiyrtvlyicassrwrhlegipqacgaetngsqflphkrefseanpagnlpkv 85
QY 71 DAD-ENSLAGELDEAGSSEWIALTKSPQAFYRGPRPSWQGTGVLGRSDVLAGLSGCC 129
Db 86 dasgedrlwg-----gqmpteeelwskhsvmsrqd-----lqtloc 122
QY 130 KWGCSKSEISLSC 142
Db 123 tdgcsmdtsalc 135
RESULT 12
AAB20110
ID AAB20110 standard; Protein; 135 AA.
XX AAB20110;
XX AC AAB20110;
XX DT 30-APR-2001 (first entry)
XX DE Human immunostimulant PRO182.
XX

CC skin diseases (such as bullous skin disease, erythema multiforme and
 CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,
 CC atopic dermatitis, food hypersensitivity and urticaria), immunologic
 CC diseases of the lung and transplantation associated diseases (such
 CC as graft rejection and graft-versus-host disease) (all claimed).
 CC Claimed methods of diagnosing these disorders comprise detecting
 CC the level of expression of the PRO gene. Also claimed are a method
 CC of identifying a compound capable of inhibiting the expression or
 CC activity of the PRO polypeptide, vectors, host cells and
 CC antibodies.

XX SQ Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 22; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

QY 32 VRLCGREFRAVIFTGCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 Db 26 vrlcglelyrtviycasswrhrhlegipqaggaetgnsfqiphkrefseenpaqlpkv 85
 QY 71 DAD-EDSLAGELDEAMGSSSEWLALTKSPQAFYGRPSWQGTGVLGRSDVLGLSSCC 129
 Db 86 dasgedrlwg-----gqmpeteelwskkhsvmsrkd-----lqtlcc 122
 QY 130 KWGCSKSEISLSC 142
 Db 123 tdgcsmtldisalc 135

RESULT 13

AAB53072
 ID AAB53072 standard; Protein; 135 AA.

AC AAB53072;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO182, SEQ ID NO:41.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.

XX OS Homo sapiens.

PN WO200053753-A2.

XX 14-SEP-2000.

PD 05-JAN-2000; 2000WO-US00219.

PF 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21050.

PR 05-OCT-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

XX Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-090793/10.

XX N-PSDB; AAC97396.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 69; Fig 18; 293pp; English.

CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a PRO protein of the
 CC invention.

XX SQ Sequence 135 AA;

Query Match 16.6%; Score 126.5; DB 22; Length 135;
 Best Local Similarity 30.8%; Pred. No. 6.1e-06;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

QY 32 VRLCGREFRAVIFTGCGSRWRR-----SDILAH-----EAMGDTFPDA 70
 Db 26 vrlcglelyrtviycasswrhrhlegipqaggaetgnsfqiphkrefseenpaqlpkv 85

QY 71 DAD-EDSLAGELDEAMGSSSEWLALTKSPQAFYGRPSWQGTGVLGRSDVLGLSSCC 129
 Db 86 dasgedrlwg-----gqmpeteelwskkhsvmsrkd-----lqtlcc 122

QY 130 KWGCSKSEISLSC 142
 Db 123 tdgcsmtldisalc 135

RESULT 14

AAP40108

ID AAP40108 standard; Protein; 185 AA.

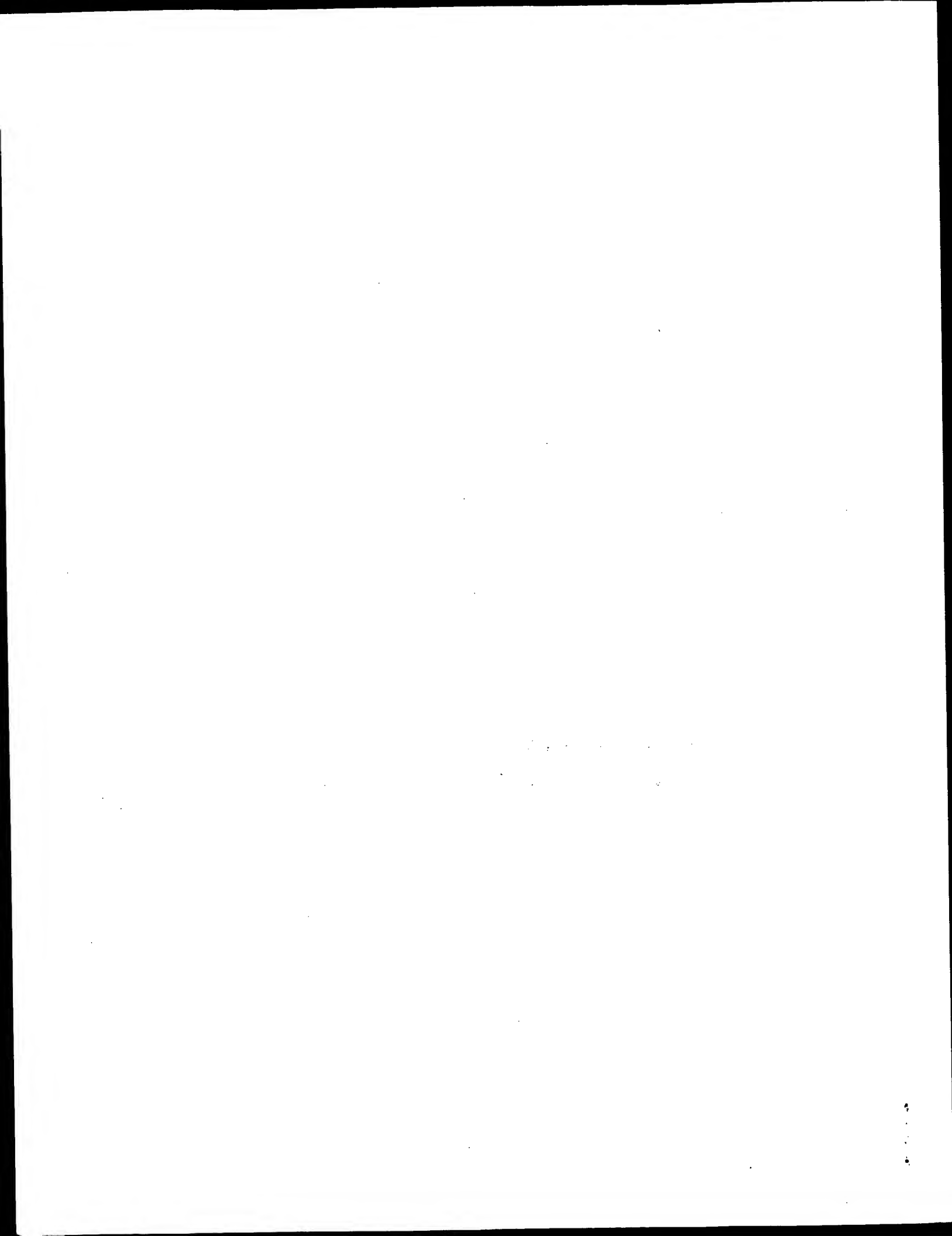
XX AC AAP40108;

• Fri Jun 28 11:32:00 2002

Search completed: June 27, 2002, 16:08:08
Job time: 277 sec

us-09-781-077-2.rag

Page 11



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:05:31 ; Search time 28.78 seconds
(without alignments)
120.515 Million cell updates/sec

Title: US-09-781-077-2
Perfect score: 760
Sequence: 1 MARYMLLLVAVLTGELW.....GLSSCKKWCCKSEISSLC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6ptodata/2/1aa/5A_COMB.pap.*
2: /cgn2_6ptodata/2/1aa/5B_COMB.pap.*
3: /cgn2_6ptodata/2/1aa/6A_COMB.pap.*
4: /cgn2_6ptodata/2/1aa/6B_COMB.pap.*
5: /cgn2_6ptodata/2/1aa/PTUS_COMB.pap.*
6: /cgn2_6ptodata/2/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 148 | 19.5 | 135 | 3 | US-08-950-720A-6 |
| 2 | 126.5 | 16.6 | 135 | 3 | US-08-950-720A-2 |
| 3 | 116 | 15.3 | 130 | 6 | 5464756-16 |
| 4 | 109.5 | 14.4 | 185 | 3 | US-08-950-720A-12 |
| 5 | 107.5 | 14.1 | 162 | 6 | 5464756-18 |
| 6 | 102.5 | 13.5 | 164 | 6 | 5464756-20 |
| 7 | 102 | 13.4 | 29 | 6 | 5464756-15 |
| 8 | 98.5 | 13.0 | 185 | 3 | US-08-950-720A-13 |
| 9 | 98 | 12.9 | 77 | 1 | US-08-443-568B-10 |
| 10 | 98 | 12.9 | 77 | 5 | PCT-US94-06997-10 |
| 11 | 95 | 12.5 | 101 | 3 | US-08-950-720A-14 |
| 12 | 92.5 | 12.2 | 40 | 2 | US-08-353-476-92 |
| 13 | 89.5 | 11.8 | 150 | 1 | US-08-443-568B-12 |
| 14 | 89.5 | 11.8 | 150 | 5 | PCT-US94-06997-12 |
| 15 | 88.5 | 11.6 | 134 | 4 | US-09-201-226-2 |
| 16 | 88.5 | 11.6 | 188 | 2 | US-08-905-267-2 |
| 17 | 88.5 | 11.6 | 188 | 4 | US-09-314-051-2 |
| 18 | 84.5 | 11.1 | 110 | 3 | US-08-950-720A-11 |
| 19 | 84.5 | 11.1 | 110 | 3 | US-08-589-028-2 |
| 20 | 84.5 | 11.1 | 110 | 3 | US-08-784-582-2 |
| 21 | 84.5 | 11.1 | 110 | 4 | US-08-785-271-2 |
| 22 | 84.5 | 11.1 | 110 | 5 | PCT-US95-08596-2 |
| 23 | 79.5 | 10.5 | 1070 | 4 | US-08-697-954-2 |
| 24 | 76 | 10.0 | 31 | 2 | US-08-484-219-4 |
| 25 | 76 | 10.0 | 213 | 2 | US-08-905-267-13 |
| 26 | 76 | 10.0 | 213 | 4 | US-09-314-051-13 |
| 27 | 74.5 | 9.8 | 24 | 6 | 5464756-8 |

| | | | | | | |
|----|------|-----|-----|---|-------------------|--------------------|
| 28 | 73 | 9.6 | 32 | 6 | 5464756-11 | Patent No. 5464756 |
| 29 | 73 | 9.6 | 33 | 6 | 5464756-10 | Patent No. 5464756 |
| 30 | 72 | 9.5 | 174 | 3 | US-08-911-853-19 | Sequence 19, Appl |
| 31 | 72 | 9.5 | 174 | 4 | US-09-479-409-19 | Sequence 19, Appl |
| 32 | 72 | 9.5 | 174 | 4 | US-09-479-453-19 | Sequence 19, Appl |
| 33 | 71.5 | 9.4 | 110 | 3 | US-08-589-028-4 | Sequence 4, Appl |
| 34 | 71.5 | 9.4 | 110 | 3 | US-08-784-582-4 | Sequence 4, Appl |
| 35 | 71.5 | 9.4 | 110 | 4 | US-08-785-271-4 | Sequence 4, Appl |
| 36 | 71 | 9.3 | 29 | 1 | US-08-443-568B-2 | Sequence 2, Appl |
| 37 | 71 | 9.3 | 29 | 2 | US-08-484-219-5 | Sequence 5, Appl |
| 38 | 71 | 9.3 | 29 | 5 | PCT-US94-06997-2 | Sequence 2, Appl |
| 39 | 71 | 9.3 | 33 | 2 | US-08-353-476-90 | Sequence 90, Appl |
| 40 | 71 | 9.3 | 52 | 1 | US-08-443-568B-14 | Sequence 14, Appl |
| 41 | 71 | 9.3 | 52 | 5 | PCT-US94-06997-14 | Sequence 14, Appl |
| 42 | 69 | 9.1 | 94 | 1 | US-07-989-845-28 | Sequence 28, Appl |
| 43 | 69 | 9.1 | 94 | 1 | US-07-989-844-12 | Sequence 12, Appl |
| 44 | 69 | 9.1 | 94 | 1 | US-08-161-044-12 | Sequence 12, Appl |
| 45 | 69 | 9.1 | 94 | 1 | US-08-240-121-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-950-720A-6

Query Match 19.5% Score 148; DB 3; Length 135;

Best Local Similarity 29.9%; Pred. No. 1.3e-09;
Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

QY 1 MARYMLLLAVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRRRSIDLAH 60
| :||:|||| | :||:|||| | :||:|||| | :||:|||| | :||:||||
Db 6 LALFLLVLLAV-----VEVRSR-QTVKLCGLDYVTVIYICASSRRRH-----49

QY 61 EAMGDTFPDADDESLAGELDEAMGSSEWL-----ALTKSPQAFYRGRPSWQ 108
| :||:|||| | :||:|||| | :||:|||| | :||:|||| | :||:||||
Db 50 --LEGHFSQQAETRNVLQLDLRHPKKTLEHSLPKTDLGQGLVRLDQAPKEG--LWE 105

QY 109 GTPGVLRGSRDVLGSLSSCKKWCCKSEISSLC 142
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Db 106 LKHVVSVRRD----LQALCCRGCSMKELSTLC 135

RESULT 2
US-08-950-720A-2
; Sequence 2, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-950-720A-2

Query Match 16.6%; Score 126.5; DB 3; Length 135;
Best Local Similarity 30.8%; Pred. No. 3.9e-07;
Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

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Db 26 VRLCGLEVIVTVIYICASSRRRHLEGIPOAQQAETGNSFQLPKHREFSEENPAQLPKV 85

QY 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQTPGVLRGSRDVLGSLSSCC 129
|| ||||| | :||:|||| | :||:|||| | :||:|||| | :||:|||| | :||:||||
Db 86 DASGEDRLWG-----GQMPTEELWKSKKHSVMSRQD-----LQTLCC 122

QY 130 KWGCSKSEISSLC 142
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Db 123 TDGCSMTDLSALC 135

RESULT 3
5464756-16
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:16:
; LENGTH: 30
5464756-16

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RESULT 4
US-08-950-720A-12
; Sequence 12, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6672

; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
; US-08-950-720A-12

Query Match 14.4%; Score 109.5; DB 3; Length 185;
Best Local Similarity 22.7%; Pred. No. 5.3e-05;
Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;
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Db 1 MPRLLFFHLLGVCLLLNQFRAVADSWMEVVKLCGRELVRQAIAICGMSWKSLSQE 60
QY 61 EAMGDTTPDADADESLAGELDEAMGSSEWLA-----LTKS-----PQ----- 98
Db 61 DAPOTPRVAEIVPSFINKDTETINMSEFVANLPQELKLTLSMQPALQOHPVPLK 120
QY 99 -----AFYGRPS-----WQGTGVLGRSDVLAGLSSCKCKWGCKSE 137
Db 121 DSSLFEEFKKLIRNROSEADSSPELKYLGLDTHSRKKRQLYSALANKCHVGCTKRS 180
QY 138 ISSIC 142
Db 181 LARFC 185

RESULT 5
5464756-18
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:18:
; LENGTH: 162
5464756-18

Query Match 14.1%; Score 107.5; DB 6; Length 162;
Best Local Similarity 23.4%; Pred. No. 7.6e-05;
Matches 36; Conservative 20; Mismatches 55; Indels 43; Gaps 4;
QY 32 VRLCGREFIRAVFTCGGSRWRSDILAHAMGDTFPDADADESLAGELDEAMGSSEWL 91
Db 9 IKLCGRELVRQAIAICGMSWKSLSQEDAPQTPRPVAEIVPSFINKDTETINMSEFV 68
QY 92 A-----LTKS-----PQ-----AFYGRPS-----WQ 108
Db 69 ANLPQELKLTLSMQPALQOHPVPLKDSLLFEEFKKLIRNROSEADSSPELKYL 128
QY 109 GTPGVLRGRSDVLAGLSSCKCKWGCKSEISLCL 142
Db 129 GLDTHSRKKRQLYSALANKCHVGCTKRLARFC 162

RESULT 6
5464756-20
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,

; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:20:
; LENGTH: 164
5464756-20

Query Match 13.5%; Score 102.5; DB 6; Length 164;
Best Local Similarity 22.4%; Pred. No. 0.00029;
Matches 35; Conservative 20; Mismatches 56; Indels 45; Gaps 4;
QY 32 VRLCGREFIRAVFTCGGSRWRSDILAHAMGDT-----FPDADADESLAGEL 81
Db 9 IKLCGRELVRQAIAICGMSWKSLSQEDAPQTPRPVAEIVPSFINKDTETINMSEF 68
QY 82 DEAMGSSEWLTKSPOA-----FYGRPS-----W 107
Db 69 VANLPQELKLTLSMQPALQOHPVPLKDSLLFEEFKKLIRNROSEADSSPELKY 128
QY 108 GTPGVLRGRSDVLAGLSSCKCKWGCKSEISLCL 142
Db 129 GLDTHSRKKRQLYSALANKCHVGCTKRLARFC 164

RESULT 7
5464756-15
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:15:
; LENGTH: 29
5464756-15

Query Match 13.4%; Score 102; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 3.4e-05;
Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 31 GVRLCGREFIRAVFTCGGSR 51
Db 9 GIKLCGREFIRAVFTCGGSR 29

RESULT 8
US-08-950-720A-13
; Sequence 13, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.

us-09-781-077-2-rai

Fri Jun 28 11:32:00 2002

```

; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
; US-08-950-720A-13

; Query Match 13.0%; Score 98.5; DB 3; Length 185;
; Best Local Similarity 23.8%; Pred. No. 0.00098;
; Matches 44; Conservative 19; Mismatches 79; Indels 43; Gaps 5;

QY 1 MARYMLLLAVVLTGELMPGAFAARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
Db 1 MFRLFLHLLFCLLLNQFSRAVAKKWDDVIKLCGRVLVRAQIATCGMSTWKSLSQE 60
QY 61 EAMGDTFFDAD-----ADEDS-----LAGELDEAMGSSEWL-----ALT 94
Db 61 DAPOTPRPVAEIVPSPFINKDTETIIIMLEFANLPPELKAALSERQPSLPQLQQYVPALK 120
QY 95 KSPQAF-----YRGRPS-----WQGTPEVLRGSRDVLGLSSCKKWCCKSGE 137
Db 121 DSNLSEFEFKLIRNRQSEADSNPSELKYLGLDTHSQKRRPYVALFEKCCCLIGCTKRS 180
QY 138 ISSLC 142
Db 181 LAKYC 185

RESULT 9
US-08-443-568B-10
; Sequence 10, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Vansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
; US-08-950-720A-13

; Query Match 13.0%; Score 98.5; DB 3; Length 185;
; Best Local Similarity 23.8%; Pred. No. 0.00098;
; Matches 44; Conservative 19; Mismatches 79; Indels 43; Gaps 5;

QY 1 MARYMLLLAVVLTGELMPGAFAARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
Db 1 MFRLFLHLLFCLLLNQFSRAVAKKWDDVIKLCGRVLVRAQIATCGMSTWKSLSQE 60
QY 61 EAMGDTFFDAD-----ADEDS-----LAGELDEAMGSSEWL-----ALT 94
Db 61 DAPOTPRPVAEIVPSPFINKDTETIIIMLEFANLPPELKAALSERQPSLPQLQQYVPALK 120
QY 95 KSPQAF-----YRGRPS-----WQGTPEVLRGSRDVLGLSSCKKWCCKSGE 137
Db 121 DSNLSEFEFKLIRNRQSEADSNPSELKYLGLDTHSQKRRPYVALFEKCCCLIGCTKRS 180
QY 138 ISSLC 142
Db 181 LAKYC 185

RESULT 9
US-08-443-568B-10
; Sequence 10, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Vansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-443-568B-10

; Query Match 12.9%; Score 98; DB 1; Length 77;
; Best Local Similarity 19.8%; Pred. No. 0.00035;
; Matches 22; Conservative 14; Mismatches 23; Indels 52; Gaps 2;

QY 32 VRLCGREFIRAVIFTCGSRWRSDILAHAMGDTFFDADADESLAGELDEAMGSSEWL 91
Db 19 IKLCGRVLVRAQIATCGMSTWSK----- 41
QY 92 ALTKPQAFYGRPSWQGTPEVLRGSRDVLGLSSCKKWCCKSGKSEISSLC 142
Db 42 ----RKPTGYGSGK-----KRQLYSALANKCHVGCTKRSLARFC 77

RESULT 10
PCF-US94-06997-10
; Sequence 10, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCF/US94/06997
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.

```


Fri Jun 28 11:32:00 2002

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Patent In Release #1.0, Version #1.25
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25, 227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06997-12

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Query Match      11.8%; Score 89.5; DB 5; Length 150;
Best Local Similarity 22.7%; Pred. No. 0.008; Indels 43; Gaps 4;
Matches 34; Conservative 18; Mismatches 55;
36 GREFRVAVFTCGGSRWRRSDILAEAMGDTFPDADADEDSLAGEIDRAGSSEWLA--- 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 GRELVRAQAIACGMSWKSRSLSQEDAPQTPRPVAEIVPSFINKDTETINMSEFVANLP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
93 ----LTKS-----PQ-----AFYGRGPS-----WOGTGP 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 QELKLILSEWQPALPOLQHPVVLKDSLLPFEFKLIIRQSEAAADSPSELKYLGLDT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
113 VLGRSDVLVAGLSSCKGWGSKSEISLC 142
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 HSRKKROLYSALANKCCHVGCTKRSLARFC 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

[illegible]

RESULT 14
PC-TUS94-06997-12
; Sequence 12, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; APPLICANT: Process for Producing Relaxin
; TITLE OF INVENTION: 37
; NUMBER OF SEQUENCES: 37

| | | | | |
|-----------------------|--------------|------------------|------------|-------------|
| Query Match | 11.6% | Score 88.5; | DB 4; | Length 134; |
| Best Local Similarity | 25.5%; | Prod. No. 0.009; | | |
| Matches 37; | Conservative | 19; | Mismatches | 60; |
| | | | Indels | 29; |
| | | | Gaps | 6; |

APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37

us-09-781-077-2.rai

Page 7

| | | | | |
|----|-----|------------------------------------------------------------|-------------------------------------|----|
| QY | 6 | LLLLLAVVLITGELWPGAEARAPYGVRLCGREFIRAVITFCGGS | ---RRRRSDILAHEA | 62 |
| Db | 10 | LLLLLLAT---ASQLQPVQGR | ---KMGCEALLQALDVICVNGFTRVRVRSASKDAR | 61 |
| QY | 63 | MGDTF-----PDADADEDSLDELDMGSSSEWIALTKSPQAFYRGRPSQOQTGVLGRGS | 117 | |
| Db | 62 | VNDLIRKLOQPDDEIQEETETGLKQKHTDAD-----TEKGVPPAVGSGRKLRRH | 111 | |
| QY | 118 | RDVLVAGLSSSCCKWGCSEISLCL | 142 | |
| Db | 112 | RRRIA---HECCKEGCTVDILDYC | 133 | |

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 16:05:56 ; Search time 36.01 Seconds
(without alignments)
378.914 Million cell updates/sec

Title: US-09-781-077-2

Perfect score: 760

Sequence: 1 MARYMLLLAVVLTGELW.....GLSSCCCKWGCSEISL 142

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|-------------------------|
| 1 | 153 | 20.1 | 54 | 2 | A26463 | relaxin - spiny dogfish |
| 2 | 117 | 15.4 | 44 | 1 | RXRKOT | relaxin - sand tiger |
| 3 | 109.5 | 14.4 | 185 | 1 | A60982 | relaxin 2 precursor |
| 4 | 108.5 | 14.3 | 166 | 2 | S42786 | relaxin 2 precursor |
| 5 | 106.5 | 14.0 | 182 | 1 | RXPQ | relaxin precursor |
| 6 | 102 | 13.4 | 131 | 2 | A53024 | Leydig insulin-like |
| 7 | 101.5 | 13.4 | 185 | 2 | A34936 | relaxin precursor |
| 8 | 100.5 | 13.2 | 64 | 2 | A29543 | relaxin - little s |
| 9 | 99 | 13.0 | 131 | 2 | B53024 | Leydig insulin-like |
| 10 | 99 | 13.0 | 185 | 2 | S48082 | relaxin precursor |
| 11 | 98.5 | 13.0 | 185 | 1 | A44559 | relaxin 1 precursor |
| 12 | 98 | 12.9 | 186 | 1 | RXPRT | relaxin precursor |
| 13 | 95.5 | 12.6 | 166 | 2 | S42783 | relaxin 1 precursor |
| 14 | 89.5 | 11.8 | 59 | 2 | A53879 | relaxin - dog (fra |
| 15 | 88 | 11.6 | 145 | 2 | S43224 | insulin-related pr |
| 16 | 86.5 | 11.4 | 57 | 2 | S42784 | relaxin - gorilla |
| 17 | 86.5 | 11.4 | 178 | 2 | A49014 | 20K protein - rabb |
| 18 | 84.5 | 11.1 | 110 | 1 | IPHU | insulin precursor |
| 19 | 83.5 | 11.0 | 110 | 2 | A42179 | insulin precursor |
| 20 | 82.5 | 10.9 | 139 | 2 | A83140 | hypothetical prote |
| 21 | 80.5 | 10.6 | 110 | 2 | JQ0178 | insulin precursor |
| 22 | 80 | 10.5 | 106 | 2 | AD0408 | conserved hypothet |
| 23 | 80 | 10.5 | 187 | 2 | T10897 | insulin-like growt |
| 24 | 78.5 | 10.3 | 54 | 2 | B32201 | relaxin - minke wh |
| 25 | 78.5 | 10.3 | 110 | 2 | B42179 | insulin precursor |
| 26 | 78 | 10.3 | 116 | 1 | IPAF | insulin precursor |
| 27 | 78 | 10.3 | 2591 | 2 | T30288 | pristinamycin I sy |
| 28 | 77 | 10.1 | 143 | 2 | I47053 | relaxin B,C and A |
| 29 | 77 | 10.1 | 2129 | 2 | T14182 | fbx protein - Myc |

| | | | | | | |
|----|------|------|------|---|--------|--------------------|
| 30 | 77 | 10.1 | 2569 | 2 | T14164 | peptide synthetase |
| 31 | 76.5 | 10.1 | 48 | 2 | A49739 | relaxin - horse (f |
| 32 | 76.5 | 10.1 | 108 | 2 | A39883 | insulin precursor |
| 33 | 76.5 | 10.1 | 115 | 1 | IPHP | insulin precursor |
| 34 | 76.5 | 10.1 | 380 | 2 | C83171 | conserved hypothet |
| 35 | 76 | 10.0 | 513 | 1 | RGECAV | transcription regu |
| 36 | 76 | 10.0 | 513 | 2 | F90866 | hypothetical prote |
| 37 | 76 | 10.0 | 513 | 2 | C85752 | conserved hypothet |
| 38 | 75.5 | 9.9 | 319 | 2 | D75349 | insulin-like growt |
| 39 | 75 | 9.9 | 193 | 2 | A53697 | probable zinc meta |
| 40 | 75 | 9.9 | 663 | 2 | C70838 | probable zinc meta |
| 41 | 75 | 9.9 | 667 | 2 | C87236 | catalase (EC 1.11. |
| 42 | 74.5 | 9.8 | 576 | 2 | S33327 | relaxin - Bryde's |
| 43 | 73.5 | 9.7 | 54 | 2 | A32201 | insulin precursor |
| 44 | 73.5 | 9.7 | 107 | 1 | IFCH | insulin precursor |
| 45 | 73 | 9.6 | 109 | 1 | IPRTDU | insulin precursor |

ALIGNMENTS

RESULT 1
A26463
relaxin - spiny dogfish (fragments)
C:Species: Squalus acanthias (spiny dogfish)
C:Date: 19-Nov-1988 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: B26463; A26463
R:Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, Eur. J. Biochem. 161, 335-341, 1986
A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias) cDNA.
A:Reference number: A91179; MUID:87054035
A:Accession: B26463
A:Molecule type: protein
A:Residues: 'E', 2-30 <BUIL>
A:Experimental source: ovary
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
A:Accession: A26463
A:Molecule type: protein
A:Residues: 31-54 <BUI>
A:Experimental source: ovary
C:Superfamily: insulin
C:Keywords: hormone; pyroglutamic acid
F:1-30/Domain: chain B #status experimental <MAT>
F:31-54/Domain: chain A #status experimental <CHB>
F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F:13-41,25-54,40-45/Disulfide bonds: #status predicted

Query Match 20.1%; Score 153; DB 2; Length 54;
Best Local Similarity 28.6%; Pred. No. 5.2e-08;
Matches 32; Conservative 10; Mismatches 4; Indels 66; Gaps 2;
QY 31 GVRLCGRFTRAVFTCGSRWRSDILAHEAMGTFPDADADESLAGELDEAMGSEW 90
Db :::::::::::::::::::::::
9 GIKLCGRFTRAVFTCGSRWRSDILAHEAMGTFPDADADESLAGELDEAMGSEW 90
QY 91 LALTKSPQAFYGRGRSFGTGVLRGRDVLGLSSCCCKWGCSEISL 142
Db :::::::::::::::
30 -----WEGSP-----GMSRCKCTGYCTRKDISILC 54

RESULT 2
RXRROT
relaxin - sand tiger (tentative sequence) (fragments)
C:Species: Odontaspis taurus (sand tiger)
C:Date: 01-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000
C:Accession: A01616
R:Gowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L.
FEBS Lett. 129, 80-82, 1981
A:Title: On the primary and tertiary structure of relaxin from the sand tiger shark
A:Reference number: A01616; MUID:82004703
A:Accession: A01616

Db 1 MPRLFFHLLGVCLLNQFSRAVADSWMEEVIKLCGRELVRQAQIATCGMSTINCRADLEGE

R; Schwabe, C.; Mcl

A; Residues: 25-50; TWGR; 161-182 <JAM>
R: Schwabe, C.; McDonald, J.K.; Steinetz, B.G.

R; SC

A;Title: Primary structure of porcine relaxin:
A;Reference number: A93187; MUID:77213067
A;Accession: A93187
A;Molecule type: protein
A;Residues: 25-50, 'TWGR', 161-182 <JAN>
A;Residual: 1 W. Steinmetz, B.G.

| Query Match | 13.4%; | Score 102; | DB 2; | Length 131; |
|-----------------------|-------------------------------------------------------------------|-----------------|-------|-----------------------------------|
| Best Local Similarity | 24.8%; | Pred. NO. 0.01; | | |
| Matches | 32; | Conservative | 19; | Mismatches 46; Indels 32; Gaps 5; |
| 23 | AEAPAAAPYGVRLCGRFFIRAVITCGSGSRWRSSDILAHEAMGDTFPDADADFDSDIAGELD 82 | | | |
| 24 | APAQEAP--EKLCGHFFHVALVRLCGPRW-----SPEGRVAVAGGDR 64 | | | |
| 83 | EAMGSSSW-----LALTKSPQAFYGRFSWOGTGPVLRGSRDVLAGLSSCCCKWGC 133 | | | |
| 65 | ELL---QWLEGQHLFHGLMASGDPMLVLAQPPPOAS-GHHHRRRAATNPARHCCLSGC 120 | | | |
| 134 | SKSEISLCL 142 | | | |
| 121 | TRODILLTLC 129 | | | |

```

RESULT 7
A34936
relaxin precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Jun-1998
C:Accession: A34936
R:Crawford, R.J.; Hammond, V.E.; Roche, P.J.; Johnston, P.D.; Tregear, G.W.
J. Mol. Endocrinol. 3, 169-174, 1989
A:Title: Structure of rhesus monkey relaxin predicted by analysis of the single-copy
A:Reference number: A34936; MUID:90073957
A:Accession: A34936
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-185 <CRA>
C:Superfamily: insulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-185/Product: relaxin #status predicted <MAT>

```

| | | | | |
|-----------------------|------------------|------------------|------------|-------------|
| Query Match | 13.4% | Score 101.5; | DB 2; | Length 185; |
| Best Local Similarity | 22.7%; | Pred. No. 0.016; | | |
| Matches | 42; Conservative | 22; Mismatches | 78; Indels | 43; Gaps 4; |

A: Molecule type: MENA
A: Crosses: 1-131 <RES>
A: Residues: 1-131
A: Crosses-refs: GB:S72482; NID:g632798; PIDN:AAB31371.1; PID:g632799
A: Gene: GDB:INSL3
A: Cross-references: GDB:230307; OMIM:146738
A: Map position: 19p13.2-19p12
A: IntrExons: 64/1

Query Match 13.0%; Score 99; DB 2; Length 131;
Best Local Similarity 25.2%; Pred. No. 0.02;
Matches 32; Conservative 12; Mismatches 37; Indels 46; Gaps

| | | | | | | | | | | | |
|----|-----|----------------------|--------------------------------------|----|-----|----------------------|--------------------------------------|----|-----|----------------------|--------------------------------------|
| QY | 89 | EWLA | -----LHQPQALHAGN | QY | 89 | EWLA | -----LHQPQALHAGN | QY | 89 | EWLA | -----LHQPQALHAGN |
| | | : | | | | : | | | | : | |
| Db | 68 | QWLERHLLHGLVADSNLTGP | -----GLQPLQTSHHHRHRAAATNPARYCCLSGCTQ | Db | 68 | QWLERHLLHGLVADSNLTGP | -----GLQPLQTSHHHRHRAAATNPARYCCLSGCTQ | Db | 68 | QWLERHLLHGLVADSNLTGP | -----GLQPLQTSHHHRHRAAATNPARYCCLSGCTQ |
| QY | 136 | SEISSLC | 142 | QY | 136 | SEISSLC | 142 | QY | 136 | SEISSLC | 142 |
| | | : | | | | : | | | | : | |
| Db | 123 | QDLTLTC | 129 | Db | 123 | QDLTLTC | 129 | Db | 123 | QDLTLTC | 129 |
| | | | result | | | | 10 | | | | 10 |

A:Title: The mouse relaxin gene: nucleotide sequence and expression.
A:Reference number: S48082; MUID:93199663
A:Accession: S48082
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <EVA>
A:Cross-references: EMBL:Z27088; NID:g414780; PTDN:CAA81611.1; PID:g414780
R:Buelllesbach, E.E.; Schwabe, C.
R:Biochem. Biophys. Res. Commun. 196, 311-319, 1993
A:Title: Mouse relaxin: synthesis and biological activity of the first r
A:Reference number: D06626; MUID:94030011

```

C:Superfamily: Insulin
C:Keywords: hormone
F:23-57,161-185/Product: relaxin #status experimental <MAY>
F:23-57/Domain: chain B #status experimental <CHB>
F:161-185/Domain: chain A #status experimental <CHA>
F:36-171,148-185,170-175/Disulfide bonds: #status experimental

Query Match 13.0% Score 99; DB 2; Length 185;
Best Local Similarity 24.7% Pred. No. 0.029;
Matches 47; Conservative 20; Mismatches 67; Indels 56; Gaps 1

QY 1 MARYMLLLLLAYVWV-----TGELWPGAEARAAPYVRLCGREFIRAVITFTCGGSR
DB 1 MSSRFLLQLLGFLLWLLSQPRTVSEEMDQ-----FIRMCGREYARELIKICASVG
QY 53 R-----RSDILAHNA-----MGDTFDPADAD-----EDSLAGEIDAMGSGSEWIA

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| | Query Match | 13.08; | Score 99; | DB 2; | Length 185; |
|----|-----------------------|----------------------------------------------------------|------------------|------------|-------------|
| | Best Local Similarity | 24.7%; | Pred. No. 0.029; | | |
| | Matches 47; | Conservative | Mismatches 67; | Indels 56; | Gaps 5; |
| Qy | 1 | MARYMLLLLAWVVL-----TGELWPGAEARAAPYVRLCGREFIRAVIFTCGGSRW | | | |
| | 1 | | | | |
| Db | 1 | MSSRFLLQLGLFWLLLSOPCTRVSSEWMDG-----FIMCGREYARELIKICGASVG | | | |
| | 1 | | | | |
| Qy | 53 | R-----RSDILAHEA--MGDTFPDAD-----EDSLAGELDAMGSSEWLA | | | |
| | 1 | | | | |
| Db | 53 | CGGATATLADGAWGVCFTWKDAFDFTTTLKCLPNLSPELKAIVLEAQASLPELQ | | | |
| | 1 | | | | |

blaxin precursor - rat
 Species: Rattus norvegicus (Norway rat)

76 - STAGE I DERMOCESTUS A. TUCKER & ...

76 -ST-1

76 -SLAGEI DEAMCSEEN Y EKCDON

Db 73 ANLPPELKAAL--SERQPSLPQQYVPALKDNLNLSFEFPFKLIRNRQSEADSNPSELK 130

QY 107 WQGTGPGVLRGSRDVLGAGLSSCKWGCSEISLSC 142

Db 131 YLGLDTHSQKRRQFPYVALFEKCCCLIGCTKRLANVC 166

RESULT 14

A53879

relaxin - dog (fragments)

C:Species: Canis lupus familiaris (dog)

C:Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995

C:Accession: B53879; A53879

R:Stewart, D.R.; Henzel, W.J.; Vandlen, R.

J. Protein Chem. 11, 247-253, 1992

A:Title: Purification and sequence determination of canine relaxin.

A:Reference number: A53879; MUID:93000391

A:Accession: B53879

A:Molecule type: protein

A:Residues: 1-35 <STE>

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:115401)

A:Accession: A53879

A:Molecule type: protein

A:Residues: 36-59 <ST2>

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:115399)

C:Superfamily: insulin

C:Keywords: hormone

F:1-35,36-59/Product: relaxin #status experimental <MAT>

F:1-35/Domain: chain B #status experimental <CHB>

F:36-59/Domain: chain A #status experimental <CHA>

F:9-46,21-59,45-50/Disulfide bonds: #status predicted

Query Match 11.8%; Score 89.5; DB 2; Length 59;

Best Local Similarity 20.7%; Pred. NO. 0.075;

Matches 23; Conservative 11; Mismatches 20; Indels 57; Gaps 2;

QY 32 VRLCGREFIRAVITFTCGGSEWRSSDLAHEAMGDTFPDADADEDSLAGEDEAMGSSEWL 91

Db 6 LKAGRDYVRLQIEVCGSSWGRK-----AGQLRE----- 35

QY 92 ALTKSPQAFYGRPSWQGTGPGVLRGSRDVLGAGLSSCKWGCSEISLSC 142

Db 36 -----DNVIMSDKCCNVGCTRRRELASRC 59

RESULT 15

S43224

insulin-related protein precursor - migratory locust

C:Species: Locusta migratoria (migratory locust)

C:Date: 28-Sep-1994 #sequence_revision 12-Apr-1996 #text_change 12-Jun-1998

C:Accession: S43224; S07774; S07773; S17851; S42153

R:Kromer-Metzger, E.; Lagueux, M.

Eur. J. Biochem. 221, 427-434, 1994

A:Title: Expression of the gene encoding an insulin-related peptide in Locusta (Insecta).

A:Reference number: S43224; MUID:94222089

A:Accession: S43224

A:Molecule type: DNA

A:Residues: 1-145 <KRO>

A:Cross-references: EMBL:Z29963

R:Lagueux, M.; Lwoff, L.; Meister, M.; Goltzene, F.; Hoffmann, J.A.

Eur. J. Biochem. 187, 249-254, 1990

A:Title: cDNAs from neurosecretory cells of brains of Locusta migratoria (Insecta, Orthoptera).

A:Reference number: S07774; MUID:90126827

A:Accession: S07774

A:Molecule type: mRNA

A:Residues: 1-131,133-145 <LAG>

A:Cross-references: EMBL:X17024; NID:99529; PID:g9530

R:Hietter, H.; van Dorsselaer, A.; Green, B.; Denoroy, L.; Hoffmann, J.; Luu, B.

Eur. J. Biochem. 187, 241-247, 1990

A:Title: Isolation and structure elucidation of a novel 5-kDa peptide from neurohaemal

A:Reference number: S07773; MUID:90126826

A:Accession: S07773

A:Molecule type: protein

A:Residues: 67-116 <HIE>

R:Hietter, H.; Li, K.W.; Bulet, P.; Lagueux, M.; Hoffmann, J.A.

Eur. J. Biochem. 201, 495-499, 1991

A:Title: Isolation and structural characterization of an insulin-related molecule, a

A:Reference number: S17851; MUID:92037603

A:Accession: S17851

A:Molecule type: protein

A:Residues: 34-64;123-143 <HET>

C:Genetics:

A:Introns: 70/1

F:1-22/Domain: signal sequence #status predicted <SIG>

F:34-64/Product: insulin-related protein chain B #status experimental <BCH>

F:67-116/Product: connecting peptide #status experimental <PEP>

F:123-143/Product: insulin-related protein chain A #status experimental <ACH>

Query Match 11.6%; Score 88; DB 2; Length 145;

Best Local Similarity 26.7%; Pred. No. 0.26;

Matches 39; Conservative 28; Mismatches 59; Indels 20; Gaps 8;

QY 6 LLLLLAVVLT-----GELWPGAEARA-APYGV-RLCGREFIRAVITFTCGGSRMRSDIL 58

Db 8 LLAVLAVCLSTATQOSDLFLSPKRSQAPQPVARYCGEKLNALKLVCRGN----YNTM 63

QY 59 AHEAMGDTFPDADADEDSLAGEDEAMGSSEWLALTKSPQAFYGRPSWQGTGPGVLRGS- 117

Db 64 FKXASQDV-SDSESDNYWGSQSDAEAAEAALPPYP---ILARPS---AGLLTGAV 116

QY 118 -RDVLAGLSSCKWGCSEISLSC 142

Db 117 FRRRTGVEFDECCRKSCSISELQTYC 142

Search completed: June 27, 2002, 16:09:27

Job time: 211 sec

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

| Result No. | Score | Query % | | Length | DB | ID | Description |
|------------|-------|---------|------|--------|--------|---------------------|-------------|
| | | Match | | | | | |
| 1 | 152.5 | 20.1 | 155 | 13 | Q9DEP8 | Q9DEP8 rana escul | |
| 2 | 104 | 13.7 | 180 | 6 | Q9MYK8 | Q9MYK8 felis silve | |
| 3 | 103.5 | 13.6 | 199 | 6 | Q9N0T9 | Q9N0T9 camelus dro | |
| 4 | 101 | 13.3 | 131 | 6 | Q9GK47 | Q9GK47 galago cras | |
| 5 | 98 | 12.9 | 131 | 6 | Q9N0T8 | Q9N0T8 dama dama (| |
| 6 | 88 | 11.6 | 131 | 6 | Q9N0Z8 | Q9N0Z8 capra hitcu | |
| 7 | 86 | 11.3 | 188 | 6 | Q9GK46 | Q9GK46 galago cras | |
| 8 | 82.5 | 10.9 | 139 | 16 | Q9HWY2 | Q9HWY2 pseudomona | |
| 9 | 81 | 10.7 | 1722 | 5 | Q9ND22 | Q9ND22 leishmania | |
| 10 | 80 | 10.5 | 187 | 13 | Q57687 | Q57687 taenopygia | |
| 11 | 80 | 10.5 | 187 | 13 | P79890 | P79890 gallus gallu | |
| 12 | 80 | 10.5 | 1429 | 10 | Q9FTA4 | Q9FTA4 arabisopsis | |
| 13 | 79 | 10.4 | 542 | 10 | Q9PE95 | Q9PE95 arabisopsis | |
| 14 | 78.5 | 10.3 | 454 | 2 | Q9KZ81 | Q9KZ81 streptomyce | |
| 15 | 78 | 10.3 | 2591 | 2 | Q54959 | Q54959 streptomyce | |
| 16 | 77.5 | 10.2 | 103 | 5 | O09209 | O09209 acrius conv | |

[illegible]

| | | | | |
|-----------------------|-------|------------------|----------------|--------------------|
| Query Match | 20.1% | Score 152.5; | DB 13; | Length 155; |
| Best Local Similarity | 27.7% | Pred. NO. 8e-08; | | |
| Matches | 49; | Conservative 21; | Mismatches 40; | Indels 67; Gaps 9; |

| | | | | |
|---|-----------------|------------------------------------|--------|----|
| 4 | YMLLLLVVYVLTGLM | PGAEARAAPYGVRLGREGFIRAVFTCGGSKWR | ----- | 54 |
| | : : : : : | : : : : : : : : : : : | | |
| 8 | FALLLTAT | -----VSDVGIIRGGRDFIVTVMSCGGSRWKRYS | PEPQGE | 60 |

Fri Jun 28 11:32:02 2002

OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20191540; PubMed=10727251;
 RA Hombach-Klonisch S., Abd-Elmalek M., Skidmore J.A., Leiser R.,
 RA Fischer B., Klonisch T.; pregnant one-humped camel.;
 RA "Ruminant relaxin in the pregnant one-humped camel."
 RL Biol. Reprod. 62:839-846(2000).
 CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL: AF254739; AAF67741.1; -;
 DR HSP; P01348; IRLX.
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1. F69BBD7E4FAA8089 CRC64;
 SQ SEQUENCE 199 AA; 22386 MW; 22386 MW;

Query Match 13.6%; Score 103.5; DB 6; Length 199;
 Best Local Similarity 18.1%; Pred. No. 0.0096;
 Matches 39; Conservative 24; Mismatches 62; Indels 91; Gaps 4;
 QY 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWR-----54
 Db 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWR-----54
 QY 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWR-----54
 Db 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWR-----54
 QY 55 -----SDLAHE-----AMG 64
 Db 55 -----SDLAHE-----AMG 64
 QY 61 PRAPKPAALPALSODKPKRLSRGPPAIEIPSSITKDAETLTMTLTPNLPOELTATLS 120
 Db 61 PRAPKPAALPALSODKPKRLSRGPPAIEIPSSITKDAETLTMTLTPNLPOELTATLS 120
 QY 65 DTFPDADADESLAG-----ELDEAMGSEWLATKSPQAFYGRPS 106
 Db 65 DTFPDADADESLAG-----ELDEAMGSEWLATKSPQAFYGRPS 106
 QY 121 ERQPSAEQPPALKDSNLFEEFKIIFDRQNEEEDSELKLNGLDKHSEK-----173
 Db 121 ERQPSAEQPPALKDSNLFEEFKIIFDRQNEEEDSELKLNGLDKHSEK-----173
 QY 107 WGTGPGVLRGSDVLGAGLSSCKGCKGSKSEISSLC 142
 Db 107 WGTGPGVLRGSDVLGAGLSSCKGCKGSKSEISSLC 142
 QY 174 -----KQQLQTLGERCCQKGSRKEMATAC 199
 Db 174 -----KQQLQTLGERCCQKGSRKEMATAC 199

RESULT 4

Q9GK47 PRELIMINARY; PRT; 131 AA.

ID Q9GK47 PRELIMINARY; PRT; 131 AA.
 AC Q9GK47;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN-LIKE PROTEIN.
 OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
 OX NCBI_TaxID=9463;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-TESTIS;
 RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
 RA "Molecular remodeling of members of the relaxin family during primate
 evolution."
 RL Mol. Biol. Evol. 0:0-0(2001).
 CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF317624; AAG42317.1; -;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 SQ SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;

Query Match 13.3%; Score 101; DB 6; Length 131;
 Best Local Similarity 24.5%; Pred. No. 0.01; Indels 60; Gaps 8;
 Matches 39; Conservative 15; Mismatches 60; Gaps 8;

QY 55 -----SDIL-----AHEAMGDTFFDADADE-----DSLAGELEAMG 86
 Db 61 RSNPNRDFLOWNLASLEDPRLNSLYAESHPAPNPFFSSLOKDDPTMEQLHGLYDILV 120
 QY 87 SSELALTKSPQAFYGRPSWGTGPGV-LRGSRDVLGAGLSSCKGCKGSKSEISSLC 142
 Db 121 TEE-----QOQVGLRMKRS--AGPALSCCQGRCTKNELMKFC 155

RESULT 2

Q9MYK8 PRELIMINARY; PRT; 180 AA.

ID Q9MYK8 PRELIMINARY; PRT; 180 AA.
 AC Q9MYK8;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RELAXIN.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99115216; PubMed=9915995;
 RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kaufold J.,
 RA Steger K., Huppertz B., Fischer B.;
 RA "Nucleic acid sequence of feline preprorelaxin and its localization
 within the feline placenta."
 RL Biol. Reprod. 60:305-311(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hombach-Klonisch S., Klonisch T.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF233688; AAF60303.1; -;
 DR HSP; P04090; GRX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 SQ SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;

Query Match 13.7%; Score 104; DB 6; Length 180;
 Best Local Similarity 22.2%; Pred. No. 0.0076;
 Matches 41; Conservative 21; Mismatches 75; Indels 48; Gaps 5;

QY 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWRSDI 57
 Db 1 MARYMLLLAVVLTGELWPGAEARAAPYVRLCGREFTRAVITCGGSRWRSDI 57
 QY 58 LAHEAMGDTFFDADADESLAGELEAMGSEWL-----ALTKSPQAFYGRPSWQ 108
 Db 58 LAHEAMGDTFFDADADESLAGELEAMGSEWL-----ALTKSPQAFYGRPSWQ 108
 QY 56 QHREPRQAPALPEIVSSITSGAEALNGMLEYIPDLQELKATLSEREPFRELQPSLK 115
 Db 56 QHREPRQAPALPEIVSSITSGAEALNGMLEYIPDLQELKATLSEREPFRELQPSLK 115
 QY 109 GP-----PGVL-----RGSRDVLGAGLSSCKGCKGSKSE 137
 Db 109 GP-----PGVL-----RGSRDVLGAGLSSCKGCKGSKSE 137
 QY 116 DSNLNEVEKSLGRQNEAQSLQSLGRSLDHSRIKRSYIRYSDRCCNVGCTRKE 175
 Db 116 DSNLNEVEKSLGRQNEAQSLQSLGRSLDHSRIKRSYIRYSDRCCNVGCTRKE 175
 QY 138 ISSLC 142
 Db 176 LADLC 180

RESULT 3

Q9N0T9 PRELIMINARY; PRT; 199 AA.

ID Q9N0T9 PRELIMINARY; PRT; 199 AA.
 AC Q9N0T9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PREPRORELAXIN.

QY 10 LAVW--VLTG-----ELWPCAARAPYGVRLCGREFIRAVITCGSRWRSDILAHEA 62
 Db 5 LSWALVGLPALVFAHPSLSLETRE---KLCGHFHVRLVRLCGGPRWS-----52
 QY 63 MGDTPDADADESLAGELDEAMGSSEW-----ALTKSPQAFYRG 103
 Db 53 -----PEAGT---SSAGGDRELL---QWLERPHLLHGLVAEHDPAVPGLOPFOASHH 101
 QY 104 RPSWQGTGVLGRSDVTLAGLSSCKKWKSCSEISSLC 142
 Db 102 -----RHHRRAATNPAAHRCCLSGCTRQDILLTLC 129

RESULT 5
 Q9N0T8 ID Q9N0T8 PRELIMINARY; PRT; 131 AA.
 AC Q9N0T8;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RELAXIN-LIKE PROTEIN.
 OS Dama dama (Fallow deer) (Cervus dama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=30532;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20150568; PubMed=10687860;
 RA Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
 RA Fischer B., Klonisch T.;
 RT "Relaxin-like factor (RLF) mRNA expression in the fallow deer.";
 RL Mol. Cell. Endocrinol. 159:147-158(2000).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF254740; AAF67742.1;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 SQ SEQUENCE 131 AA; 14406 MW; EC7731679E6B0C7 CRC64;

Query Match 12.9%; Score 98; DB 6; Length 131;
 Best Local Similarity 27.7%; Pred. No. 0.021;
 Matches 36; Conservative 17; Mismatches 43; Indels 34; Gaps 7;

QY 23 AEARAPYGVRLCGREFIRAVITCGSRWRSDILAHEAMGDTFPDADADES---LAG 79
 Db 24 AAQOEV---EKLCGHFHVRLVRLCGGPRW-----SSEDRRPVAGGDRLLRNLEG 72
 QY 80 E--LDEAMGSSE---WALTKSPQA--FYGRPSWQGTGVLGRSDVTLAGLSSCKKWK 132
 Db 73 QHLLHGLMASGDPVLVLAPOPLPQASRRHHRRATAINP-----ARHCCLSG 119
 QY 133 CSKSEISSLC 142
 Db 120 CTRODILLTLC 129

RESULT 6
 Q9N0Z8 ID Q9N0Z8 PRELIMINARY; PRT; 131 AA.
 AC Q9N0Z8;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RLF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=99260294; PubMed=10331451;
 RA Hombach-Klonisch S., Tetens F., Kauffold J., Steger K., Fischer B.,
 RA Klonisch T.;
 RT "Molecular cloning and localization of caprine relaxin-like factor
 (RLF) mRNA within the goat testis.";
 RL Mol. Reprod. Dev. 53:135-141(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Hombach-Klonisch S., Klonisch T.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF233686; AAF60301.1; -;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 SQ SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;

Query Match 11.6%; Score 88; DB 6; Length 131;
 Best Local Similarity 21.4%; Pred. No. 0.22;
 Matches 33; Conservative 14; Mismatches 25; Indels 82; Gaps 5;

QY 23 AEARAPYGVRLCGREFIRAVITCGSRWRSDILAHEAMGDTFPDADADESLAGELD 82
 Db 24 AAQOEV---EKLCGHFHVRLVRLCGGPRW-----51
 QY 83 EAMGSSEWALTKSPQAFYGRPSWQGTGVLGR---GSRDVLGLSSS-----127
 Db 52 -----SSE-----SGRPVAGGDRLLRNLEGQHLHGLMASGDPVLVLAPOPLP 95
 QY 128 -----CCKWGSCKSEISSLC 142
 Db 96 QASRRHHRRATAINPARHCCCLSGCTRODILLTLC 129

RESULT 7
 Q9GK46 ID Q9GK46 PRELIMINARY; PRT; 188 AA.
 AC Q9GK46;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE PRORELAXIN.
 OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
 OX NCBI_TaxID=9463;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EMBRYONIC TROPHOBLAST, PLACENTA;
 RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
 RT "Molecular remodeling of members of the relaxin family during primate
 evolution.";
 RL Mol. Biol. Evol. 0:0-0(2001).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF317625; AAG42318.1; -;
 DR HSP; P04090; 6RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 SQ SEQUENCE 188 AA; 21573 MW; 77551629B82B9A66 CRC64;

Query Match 11.3%; Score 86; DB 6; Length 188;
 Best Local Similarity 21.3%; Pred. No. 0.52;
 Matches 43; Conservative 21; Mismatches 64; Indels 74; Gaps 8;

QY 1 MARYMLLLLVVLTGELWPGAFARA-APYGVRL-----CGREFIRAVIFTCG--GSR 51
DB 1 MPRLLFFHLGVLLLTQI-----SRKMDKNGENLQIIPACGRRLIRLWVEVCGSTGER 55
QY 52 WRRSDILAH-----EAMGDTFFPDADADESLAGELDEAMGSSWELATKSPQAFYRG 103
DB 56 GRANKOTEHQPGSEFPSEIYVSPFINKDAETINN-----MSEFIANLPQKOKTTQS 106
QY 104 R-----PSWQCTPGVLGRS-----RDV 120
DB 107 EMNLPSPLOQYPTPLKSGDISFEYKNNHNEQGEADNSHSELQNLGLDTHSRKKRER 166
QY 121 LAGLSSCKCKGCKSEISSIC 142
DB 167 YMSPLQKCCRIGCTKRSIARFC 188
RESULT 8
Q9HWY2 PRELIMINARY; PRT; 139 AA.
AC Q9HWY2
DT 01-MAR-2001 (Tremblrel. 15, Created)
DT 01-MAR-2001 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN PA4046.
GN PA4046.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Carber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AF004821; AAG07433.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 139 AA; 15161 MW; 9F5D69D2981A389A CRC64;
Query Match 10.9%; Score 82.5; DB 16; Length 139;
Best Local Similarity 26.0%; Pred. No. 0.83; Indels 27; Gaps 4;
Matches 34; Conservative 14; Mismatches 56;
QY 6 LLLLLLVVLTGELWPGAFARAAPYGVRLCGREFIRAVIFTCGSRWRRSDILAHEAMGD 65
DB 22 LPLLIIVFEFLEQLPLHGLAMPFIALLSMFVNPLF---GAYKRLIATQKA--- 74
QY 66 TFPDADADESLAGELDEAMGSEW--LALTKSPQAFYRGPSWQGPV---LRGRDV 120
DB 75 -----LDTAEAAWTRIAQVRRKRALFGALSPAWIGVPGFAGLNGVALI 119
QY 121 LAGLSSCKCKW 131
DB 120 LLGVTSLVLFW 130
RESULT 9
Q9ND22 PRELIMINARY; PRT; 1722 AA.
AC Q9ND22
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE POSSIBLE SERINE PROTEASE.
GN L4325.06.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=FRIEDLIN;
RA Oliver K., Harris D., Ivens A.C., Quail M., Rajandream M.A.,
Barrell B.G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL356713; CAB92392.1; -.
DR MEROPS; S08.UPW; -.
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 2.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1722 AA; 182741 MW; 8148DD78AC52DD1F CRC64;
Query Match 10.7%; Score 81; DB 5; Length 1722;
Best Local Similarity 24.4%; Pred. No. 23;
Matches 32; Conservative 15; Mismatches 40; Indels 44; Gaps 7;
QY 10 LAVVVLGEL---WPGAARAAPYGVRLCGREFIRAVIFTCGSRWRRSDILAHEAMGD 66
DB 1507 LLLMLHTNLHWRWDSALQ-----CEARRWARA---RHRSTADT 1543
QY 67 FPDADA-DEDSLAGEAMGSSR-----WLALTKSPQAFYRGPSW--OGTP 111
DB 1544 TPGADSVGVDRKAANFDEVLGTAFRAHVGVVGRWLWASLVESTE---RDAASFVEGPE 1600
QY 112 GVLGRSRLVA 122
DB 1601 DETRFQDYAA 1611
RESULT 10
O57687 PRELIMINARY; PRT; 187 AA.
AC O57687
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE IGF-II PRECURSOR.
GN IGF-2.
OS Taenopygia guttata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeridae;
OC Taenopygia.
OX NCBI_TaxID=72052;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Holzenberger M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RX MEDLINE=97426547; PubMed=9278533;
RA Holzenberger M., Jarvis E.D., Chang C., Grossman M., Nottebohm F.,
Scharff C.;
RT "Selective expression of insulin-like growth factor II in the song
bird brain.";


```

RL J. Neurosci. 17:6974-6987(1997).
CC -|- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
DR EMBL: AJ223165; CAA11145.1; -.
DR HSSP: P01344; IGF2
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR PRINTS: PR00276; INSULIN.
DR PRINTS: PR00277; INSULINB.
DR ProDom: PD001048; Insulin_IGF_relaxin; 1.
DR SMART: SM00078; IIGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW SIGNAL.
FT CHAIN
FT CHAIN
SQ SEQUENCE 187 AA; 20908 MW; 3C7EADABF7D2CE8F CRC64;

Query Match
Best Local Similarity 23.1%; Score 80; DB 13; Length 187;
Matches 33; Conservative 8; Mismatches 38; Indels 64; Gaps 4;

QY 2 ARYMLLLAVVLTGELWPGAEARAAPYGV--RLCGREFIRAVITCGGSRWRSDILA 59
Db 11:|||||
4 ARMLLLLAFLAY-----AMDSAAAYGTAETLCGGELVDTLQFVCG----- 45
QY 60 HEAMGDTFPDADADESLAGELDEAMSGSEWIALTKSPQAFYGRPSWQGTGVLGRSD 119
Db 46 -----DRGFYFSRP-----VGRNRR 61

QY 120 VLGLSSCCCKGCKSKSEISLC 142
Db 62 FNRGIVECCFRSCDLALLELYC 84

RESULT 11
ID P79890 PRELIMINARY; PRT; 187 AA.
AC P79890;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE PREPRO-INSULIN-LIKE GROWTH FACTOR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96397665; PubMed=8804558;
RA Darling D.C., Brickell P.M.;
RT "Nucleotide sequence and genomic structure of the chicken insulin-like
growth factor-II (IGF-II) coding region.";
RL Gen. Comp. Endocrinol. 102:283-287(1996).
CC -|- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL: S82962; BAB46818.1; -.
DR EMBL: S82960; BAB46818.1; JOINED.
DR HSSP: P01344; IGF2.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR PRINTS: PR00276; INSULIN.
DR PRINTS: PR00277; INSULINB.
DR ProDom: PD001048; Insulin_IGF_relaxin; 1.
DR SMART: SM00078; IIGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
SQ SEQUENCE 187 AA; 20837 MW; B301581CD4878EEC CRC64;

Query Match
Best Local Similarity 22.4%; Score 80; DB 13; Length 187;
Matches 32; Conservative 10; Mismatches 37; Indels 64; Gaps 4;

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QY 2 ARYMLLLAVVLTGELWPGAEARAAPYGV--RLCGREFIRAVITCGGSRWRSDILA 59
Db 11:|||||
4 ARQILLLLLAFLAY-----ALDSAAAYGTAETLCGGELVDTLQFVCG----- 45
QY 60 HEAMGDTFPDADADESLAGELDEAMSGSEWIALTKSPQAFYGRPSWQGTGVLGRSD 119
Db 46 -----DRGFYFSRP-----VGRNRR 61

QY 120 VLGLSSCCCKGCKSKSEISLC 142
Db 62 INRGIVECCFRSCDLALLELYC 84

RESULT 12
ID Q9FLA4 PRELIMINARY; PRT; 1429 AA.
AC Q9FLA4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE POLYPROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=COLUMBIA;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
features of the regions of 1,381,565 bp covered by twenty one
physically assigned pl and TAC clones.";
RL DNA Res. 5:131-145(1998).
DR EMBL: AB010693; BAB10876.1; -.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00665; rve; 1.
DR Pfam: PF00098; zf_CCHC; 1.
DR SMART: SM00343; Znf_C2HC; 1.
DR zinc-finger.
KW zinc-finger.
SQ SEQUENCE 1429 AA; 159492 MW; 7B20CCFBIA9BC263 CRC64;

Query Match
Best Local Similarity 10.5%; Score 80; DB 10; Length 1429;
Matches 39; Conservative 16; Mismatches 39; Indels 56; Gaps 8;

QY 22 GAERAAAPYGVRLCGREFIRAVITCGGSRWRSDILAHEAMGDTFPDADADES----- 76
Db 1151 GIEATRTSRGLHLMQRIY-----TDLKKHNMMLDTPVSTPSPKLSL 1196
QY 77 LAG-ELDEA-----MGSEWIALTKSPQAF-----YRGPS-----WQGTGVLGRSD 119
Db 1197 LSGTALDDATEYRTVLGSLQYLAFTPDIAFAVNRLSQFMRPTNEHWOAKRIILR----- 1252
QY 120 VLGLSS-----SCCKWGC 133
Db 1253 YLAGTSHGIFLRSDFLTTHAFSDADWGC 1282

RESULT 13
ID Q9FF95 PRELIMINARY; PRT; 542 AA.
AC Q9FF95;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SIMILARITY TO UNKNOWN PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).

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SQ SEQUENCE 434 AA, 4750, 100, 2

|| : || | | :

005 *****CREDIT ADVISORY 241

db 225 LRRASAGPEVLAGLDA 241

Fri 'Jun '28 11:32:02 2002

us-09-781-077-2.rspt

Page 7

Search completed: June 27, 2002, 16:16:28
Job time: 497 sec

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:46 ; Search time 18.68 Seconds
(without alignments)
294.335 Million cell updates/sec

Title: US-09-781-077-2

Perfect score: 760

Sequence: 1 MARYMLLLVAVLTGLW.....GLSSCCCKWCKSKSEISSLC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------------|---------------------|
| 1 | 153 | 20.1 | 54 | 1 RELX_SQUAC | P11953 squalus aca |
| 2 | 148 | 19.5 | 135 | 1 INL5_MOUSE | O9yug6 mus musculus |
| 3 | 126.5 | 16.6 | 135 | 1 INL5_HUMAN | O9y506 homo sapien |
| 4 | 117 | 15.4 | 44 | 1 RELX_ODOTA | P01349 odontaspis |
| 5 | 112.5 | 14.8 | 177 | 1 RELX_CANFA | O9trm8 canis faml |
| 6 | 110 | 14.5 | 182 | 1 RELX_HORSE | F22969 equus cabal |
| 7 | 109.5 | 14.4 | 185 | 1 REL2_HUMAN | P04090 homo sapien |
| 8 | 108.5 | 14.3 | 166 | 1 REL2_PANTR | P51455 pan troglod |
| 9 | 106.5 | 14.0 | 182 | 1 RELX_PIG | P01348 sus scrofa |
| 10 | 103.5 | 13.6 | 132 | 1 INL3_BOVIN | O77801 bos taurus |
| 11 | 102 | 13.4 | 131 | 1 INL3_PIG | P51461 sus scrofa |
| 12 | 101.5 | 13.4 | 131 | 1 INL3_CALJA | O97937 callithrix |
| 13 | 101.5 | 13.4 | 185 | 1 RELX_MACMU | P19884 macaca mulla |
| 14 | 100.5 | 13.2 | 64 | 1 RELX_RAJER | P11952 raja erinac |
| 15 | 100.5 | 13.2 | 105 | 1 INL3_RAT | O9yuk0 mus musculus |
| 16 | 100 | 13.2 | 122 | 1 INL3_MOUSE | O09107 mus musculus |
| 17 | 99 | 13.0 | 131 | 1 INL3_HUMAN | P51460 homo sapien |
| 18 | 99 | 13.0 | 185 | 1 RELX_MOUSE | P47932 mus musculus |
| 19 | 98.5 | 12.9 | 186 | 1 RELX_RAT | P04808 homo sapien |
| 20 | 98 | 12.9 | 166 | 1 REL1_PANTR | P01347 rattus norv |
| 21 | 95.5 | 12.6 | 134 | 1 INL1_PANTR | P51454 pan troglod |
| 22 | 88.5 | 11.6 | 134 | 1 INL1_DROME | O9vt53 drosophila |
| 23 | 88.5 | 11.6 | 188 | 1 INL6_RAT | O9wv41 rattus norv |
| 24 | 88 | 11.6 | 145 | 1 LIIRP_LOCOMI | P15131 locusta mig |
| 25 | 88 | 11.6 | 191 | 1 INL6_MOUSE | O9y005 mus musculus |
| 26 | 86.5 | 11.4 | 177 | 1 RELX_MESAU | O64171 mesocricetu |
| 27 | 86.5 | 11.4 | 178 | 1 RELH_RABIT | P51456 oryctolagus |
| 28 | 84.5 | 11.1 | 110 | 1 INS_HUMAN | P01308 homo sapien |
| 29 | 83.5 | 11.0 | 110 | 1 INS_PANTR | P30410 pan troglod |
| 30 | 81.5 | 10.7 | 108 | 1 INS_PIG | P01315 sus scrofa |
| 31 | 80.5 | 10.6 | 110 | 1 INS_MACFA | P30406 macaca fasc |
| 32 | 80.5 | 10.6 | 113 | 1 INS_ORENI | P81025 oreochromis |
| 33 | 80 | 10.5 | 213 | 1 INL6_HUMAN | O9y581 homo sapien |

| | | | | | |
|----|------|------|-----|--------------|--------------------|
| 34 | 78.5 | 10.3 | 54 | 1 RELX_BALAC | P11184 balaenopter |
| 35 | 78.5 | 10.3 | 110 | 1 INS_CERAE | P30407 cercopithec |
| 36 | 78 | 10.3 | 116 | 1 INS_LOPPI | P01341 lophius pis |
| 37 | 76.5 | 10.1 | 108 | 1 INS_AOTTR | P10604 aotus trivi |
| 38 | 76.5 | 10.1 | 115 | 1 INS_MXGL | P01342 myxine glut |
| 39 | 76 | 10.0 | 513 | 1 TYRR_ECOLI | P07604 escherichia |
| 40 | 74.5 | 9.8 | 576 | 1 CATA_RHOCA | P37743 rhodobacter |
| 41 | 73.5 | 9.7 | 54 | 1 RELX_BALED | P11185 balaenopter |
| 42 | 73.5 | 9.7 | 107 | 1 INS_CHICK | P11332 gallus gall |
| 43 | 73.5 | 9.7 | 170 | 1 ISPF_STRCO | O910q7 streptomyce |
| 44 | 73 | 9.6 | 109 | 1 INS_OCTDE | P17715 octodon deg |
| 45 | 72 | 9.5 | 180 | 1 MPI7_LYNST | P91797 lymnaea sta |

ALIGNMENTS

RESULT 1
RELX_SQUAC
ID RELX_SQUAC STANDARD; PRT; 54 AA.
AC P11953;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP TISSUE=Ovary;
RC MEDLINE=87054035; PubMed=3780747;
RX Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
RA Callard I.P.;
RT "Isolation, purification, and the sequence of relaxin from spiny
dogfish (Squalus acanthias).";
RL Eur. J. Biochem. 161:335-341(1986).
CC -!- FUNCTION: THE FUNCTION OF RELAXIN IN AN OVIPAROUS SPECIES IS NOT
YET KNOWN.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR; A26463; A26463.
DR PIR; B26463; B26463.
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 30 RELAXIN B CHAIN.
FT NON_CONS 30 31
FT CHAIN 31 54 RELAXIN A CHAIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 13 41 INTERCHAIN.
FT DISULFID 25 54 INTERCHAIN.
FT DISULFID 40 45
SQ SEQUENCE 54 AA; 5910 MW; 1B7206773AD32A5B CRC64;

Query Match 20.1%; Score 153; DB 1; Length 54;
Best Local Similarity 28.6%; Pred No. 1.3e-08;
Matches 32; Conservative 10; Mismatches 4; Indels 66; Gaps 2;
QY 31 GVRLCGREFRAVIFTCGSRWRSSDILAHEAMGDTFPDADADESLAGELDEAMGSSEW 90
Db |:::|||||:::|||||
9 GIKLCGREFRAVIYTCGSR-----
QY 91 LALTKSPQAFYGRPSWGCTPGVLRGRDVLACLSKCKWCKSKSEISSLC 142
Db |:::|||||:::|||||
30 -----WEGSP-----GMSKCKCTGCTRKDITSLC 54

Query Match 19.5%; Score 148; DB 1; Length 135;
 Best Local Similarity 29.9%; Pred. No. 1,le-07;
 Matches 46; Conservative 21; Mismatches 51; Indels 36; Gaps 6;

1 MARYMLLLVAVVLTGELWPGAEARAAPYGVRLCGREFIRAVITCGSRWRSDILAH 60
 6 LALELLVAVVLTGELWPGAEARAAPYGVRLCGREFIRAVITCGSRWRSDILAH 60
 61 EAMGDTFDDADDEDSLAGELDAMGSSEWL-----ALTKSQAQAFYGRPSWQ 108
 50 --LEGHFHQQAETRYNQLLDREHPSKTLHSLPKTDLSELVDRDQAQKEG--LWE 105
 109 GTPGVLRGSRDVLGAGLSGCCCKGCKSKSEISLC 142
 106 LKXSVVSRD-----LQALCCREGCKMKELSTLC 135

RESULT 3

INLS_HUMAN

ID INLS_HUMAN STANDARD; PRT; 135 AA.

AC Q9Y506;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).

GN INSL5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE-Colon;

RX MEDLINE=99389725; PubMed=10458910;

RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,

RA Lok S., Jaspers S.;

RT "Identification of INSL5, a new member of the insulin superfamily.";

RL Genomics 60:50-56(1999).

CC -1- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC

CC DEVELOPMENT AND REGULATION.

CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO

CC DISULFIDE BONDS (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS

CC IN THYMUS. MINIMAL LEVELS IN TESTIS.

CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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CC EMBL; AF133817; AAD29687.1; -

CC MIN; 606413; -

CC InterPro; IPR000739; Insulin_IGF_relaxin.

CC SMART; SM00078; ILGF; 1.

CC PROSITE; PS00262; INSULIN; 1.

CC Insulin family; Hormone; Signal.

KW SIGNAL

FT CHAIN 1 18

FT CHAIN 19 48

FT CHAIN 114 135

FT CHAIN 115 135

FT CHAIN 114 135

FT CHAIN 115 135

FT CHAIN 114 135

FT CHAIN 115 135

FT CHAIN 114 135

FT CHAIN 115 135

FT CHAIN 114 135

FT CHAIN 115 135

FT CHAIN 114 135

FT CHAIN 115 135

SQ SEQUENCE 135 AA; 15524 MW; 05FF9A0F613DBF92 CRC64;

Query Match 16.6%; Score 126.5; DB 1; Length 135;
 Best Local Similarity 30.8%; Pred. No. 1.3e-05;
 Matches 41; Conservative 8; Mismatches 39; Indels 45; Gaps 5;

QY 32 VRLCGREFIRAVITCGGSRWR--SDILAH-----EAMGDTFPA 70
 DB 26 VRLCGLEYIRTVIYICASSRRHLEGIPOAQAGTGNFOLPHKRFSEENPAQNLPKV 85
 QY 71 DAD-EDSLAGELDEAMGSENLATKSPQAFYRGRPSWQGTGVLGRSDVLAGLSSCC 129
 DB 86 DASGEDRLWG-----GOMPTLELMKSKHVSMSRQD-----LQPLCC 122
 QY 130 KWCCKSEISLSC 142
 DB 123 TDGCSMTDLALC 135

RESULT 4
 ID RELX_ODOTA STANDARD; PRT; 44 AA.
 AC P01349;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Relaxin (Fragments)
 OS Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniiformes; Odontaspidae;
 OC Carcharias.
 OC NCBI_TaxID=30501;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82004703; PubMed=727472;
 RA Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.;
 RT "On the primary and tertiary structure of relaxin from the sand tiger
 shark (Odontaspis taurus).";
 RL FEBS Lett. 129:80-82(1981).
 RN [2]
 RP REVISION TO 20.
 RX MEDLINE=87054035; PubMed=3780747;
 RA Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
 RA Callard I.P.;
 RT "Isolation, purification, and the sequence of relaxin from spiny
 dogfish (Squalus acanthias).";
 RL Eur. J. Biochem. 161:335-341(1986).
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR PIR: A01616; RXRROT.
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; ILGF: 1.
 DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone.
 FT CHAIN 1 2
 FT NON-CONS 1 20 RELAXIN B CHAIN.
 FT CHAIN 20 21
 FT CHAIN 21 44
 FT MOD_RES 1 1 PTEROLIDONE CARBOXYLIC ACID.
 FT DISULFID 3 31 RELAXIN A CHAIN.
 FT DISULFID 15 44 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 30 35 INTERCHAIN (BY SIMILARITY).
 SQ SEQUENCE 44 AA; 4730 MW; 6122F6604C660607 CRC64;

Query Match 15.4%; Score 117; DB 1; Length 44;
 Best Local Similarity 24.5%; Pred. No. 3.3e-05;
 Matches 27; Conservative 6; Mismatches 11; Indels 66; Gaps 1;

QY 33 RLCGRFIRAVITCGGSRWRSDILAHAMGDTFPADEDSLAGEDEAMGSESLA 92
 :||||| ||||| ||||| |||||

Db 1 QLCGRGFIIRAITFACGGSRWATS----- 23
 QY 93 LTKSPQAFYRGRPSWQGTGVLGRSDVLAGLSSCKWCKSKSEISLSC 142
 DB 24 -----PAMSIKCCYIGCTKKDKDISVLC 44

RESULT 5
 ID RELX_CANFA STANDARD; PRT; 177 AA.
 AC Q9TRM8; Q9TRM9; Q9N027;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Prorelaxin precursor.
 GN RLN
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99150177; PubMed=10026098;
 RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
 RA Steger K., Steinetz B.G., Fischer B.;
 RT "Canine prorelaxin: nucleic acid sequence and localization within
 the canine placenta";
 RL Biol. Reprod. 60:551-557(1999).
 RN [2]
 RP SEQUENCE OF 26-60 AND 154-177.
 RC TISSUE=Placenta;
 RX MEDLINE=93000391; PubMed=1388669;
 RA Stewart D.R., Henzel W.J., Vandlen R.;
 RT "Purification and sequence determination of canine relaxin.";
 RL J. Protein Chem. 11:247-253(1992).
 CC -!- FUNCTION: Relaxin is an ovarian hormone that acts with estrogen
 CC to produce dilatation of the birth canal in many mammals.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF233687; AAF60302.1; -
 DR HSSP: P01348; 4RLX.
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; Insulin; 1.
 DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 60 RELAXIN B CHAIN.
 FT PROPEP 63 149 CONNECTING PEPTIDE (BY SIMILARITY).
 FT CHAIN 154 177 RELAXIN A CHAIN.
 FT DISULFID 34 164 INTERCHAIN.
 FT DISULFID 46 177 INTERCHAIN.
 FT DISULFID 163 188
 FT CONFLICT 49 49 I -> S (IN REF. 2).
 SQ SEQUENCE 177 AA; 20563 MW; 220BB0EC99DD302A CRC64;

Query Match 14.8%; Score 112.5; DB 1; Length 177;
 Best Local Similarity 21.5%; Pred. No. 0.00041;
 Matches 43; Conservative 16; Mismatches 60; Indels 81; Gaps 4;

Fri Jun 28 11:32:02 2002

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DR InterPro; IPR000739; Insulin_IGF_relxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 25
FT CHAIN 26 53 RELAXIN B CHAIN.
FT PROPEP 54 156 CONNECTING PEPTIDE.
FT CHAIN 161 182 RELAXIN A CHAIN.
FT DISULFID 35 169 INTERCHAIN (BY SIMILARITY).
FT DISULFID 47 182 INTERCHAIN (BY SIMILARITY).
FT DISULFID 168 173 BY SIMILARITY.
FT CONFLICT 66 66 A -> V (IN REF. 2).
FT CONFLICT 133 133 L -> Q (IN REF. 2).
SQ SEQUENCE 182 AA; 20721 MW; E5C941430A838B8 CRC64;

Query Match 14.5%; Score 110; DB 1; Length 182;
Best Local Similarity 21.8%; Pred. No. 0.00074;
Matches 41; Conservative 25; Mismatches 70; Indels 52; Gaps 6;

QY 1 MARYMLLLLVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
DB 1 MRRLFLSHVGLNLLLSQLPRELSGQKPDVVKACGRELARLRIEICGSLSKWKTVLRL 60
QY 61 EAMGDTFPDADADE-----DSLAGELDAMGSSEWL--ALTKSPQAFYRGR-PSW----- 107
DB 61 E-----PGLEAGOPVEIVSSISKDAEALNTKGLNSLNLEPKQKATLSERQPSWRELLQ 114
QY 108 -----QGTPGVLRGRSDV-----LAGLSSSCCKWGCS 134
DB 115 QPALKDSNLEEFEEETILKTQSEVEDDLSLKNLGLDKHRSKRMQLSHKCCYWGCT 174
QY 135 KSEISLCL 142
DB 175 RKELARQC 182

RESULT 7
REL2_HUMAN STANDARD; PRT; 185 AA.
ID REL2_HUMAN
AC P04090; Q9UCX3; Q99936;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prolaxin H2 precursor.
GN RN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=85051298; PubMed=6548702;
RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
RA Gorman J., Tregear G., Shine J., Niall H.;
RA "Relaxin gene expression in human ovaries and the predicted structure
RT of a human preprorelaxin by analysis of cDNA clones.";
RL EMBO J. 3:2333-2339(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Sehra H.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnarsen J.M., Fu P., Roche P.J., Tregear G.W.;
RA "Expression of human relaxin genes: characterization of a novel
RT alternatively spliced human relaxin mRNA species.";
RL Mol. Cell. Endocrinol. 118:85-94(1996).
RN [4]

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DR InterPro; IPR000739; Insulin_IGF_relxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 25
FT CHAIN 26 53 RELAXIN B CHAIN.
FT PROPEP 54 156 CONNECTING PEPTIDE.
FT CHAIN 161 182 RELAXIN A CHAIN.
FT DISULFID 35 169 INTERCHAIN (BY SIMILARITY).
FT DISULFID 47 182 INTERCHAIN (BY SIMILARITY).
FT DISULFID 168 173 BY SIMILARITY.
FT CONFLICT 66 66 A -> V (IN REF. 2).
FT CONFLICT 133 133 L -> Q (IN REF. 2).
SQ SEQUENCE 182 AA; 20721 MW; E5C941430A838B8 CRC64;

Query Match 14.5%; Score 110; DB 1; Length 182;
Best Local Similarity 21.8%; Pred. No. 0.00074;
Matches 41; Conservative 25; Mismatches 70; Indels 52; Gaps 6;

QY 1 MARYMLLLLVVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGSRWRSDILAH 60
DB 1 MRRLFLSHVGLNLLLSQLPRELSGQKPDVVKACGRELARLRIEICGSLSKWKTVLRL 60
QY 61 EAMGDTFPDADADE-----DSLAGELDAMGSSEWL--ALTKSPQAFYRGR-PSW----- 107
DB 61 E-----PGLEAGOPVEIVSSISKDAEALNTKGLNSLNLEPKQKATLSERQPSWRELLQ 114
QY 108 -----QGTPGVLRGRSDV-----LAGLSSSCCKWGCS 134
DB 115 QPALKDSNLEEFEEETILKTQSEVEDDLSLKNLGLDKHRSKRMQLSHKCCYWGCT 174
QY 135 KSEISLCL 142
DB 175 RKELARQC 182

RESULT 7
REL2_HUMAN STANDARD; PRT; 185 AA.
ID REL2_HUMAN
AC P04090; Q9UCX3; Q99936;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prolaxin H2 precursor.
GN RN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=85051298; PubMed=6548702;
RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
RA Gorman J., Tregear G., Shine J., Niall H.;
RA "Relaxin gene expression in human ovaries and the predicted structure
RT of a human preprorelaxin by analysis of cDNA clones.";
RL EMBO J. 3:2333-2339(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Sehra H.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnarsen J.M., Fu P., Roche P.J., Tregear G.W.;
RA "Expression of human relaxin genes: characterization of a novel
RT alternatively spliced human relaxin mRNA species.";
RL Mol. Cell. Endocrinol. 118:85-94(1996).
RN [4]

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DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; Insulin; 1.
 DR SMART: SM00078; ILGF; 1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 56 RELAXIN B CHAIN.
 FT PROPEP 57 154 CONNECTING PEPTIDE.
 FT CHAIN 161 182 RELAXIN A CHAIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 34 169 INTERCHAIN.
 FT DISULFID 46 182 INTERCHAIN.
 FT DISULFID 168 173
 FT CONFLICT 47 47
 FT CONFLICT 51 54 G -> GVWS (IN REF. 4).
 FT CONFLICT 116 116 WGR -> TWGR (IN REF. 3).
 FT CONFLICT 170 170 S -> L (IN REF. 1).
 FT CONFLICT 170 170 O -> E (IN REF. 6).
 SQ SEQUENCE 182 AA; 20818 MW; 20736EB089F13AB4 CRC64;

Query Match 14.0%; Score 106.5; DB 1; Length 182;
 Best Local Similarity 21.7%; Pred. No. 0.0016;
 Matches 39; Conservative 22; Mismatches 68; Indels 51; Gaps 3;
 QY 9 LLVWVLTGELWPGAEARAAPYGVRLCGREFIRAVITCGGSRWRRSDILAHEAMGDTFP 68
 DB 8 LLGWLLLSQLPREIPQSTNDFTKAGRELVLWVEICGVSWSGRTALSLEPQLETGP 67
 QY 69 DADA-----DEDSLAGEIDAMSGSEWALTKSPQAFYGRPSWQ----- 108
 DB 68 PAETMPSSITKDAEILKMWLEFVNPQLKATLSR-----QPSLRELQOSASKDSNIN 122
 QY 109 -----GTPGVLRGSRDVLGLSSCCCKWGCSSKSISSIC 142
 DB 123 FEFEKKIILNRQNEAEKSLLELKNLGLDKHSRKRRLFRMTLSEKCCQGVGKIRKDIALC 182

RESULT 10
 INL3_BOVIN STANDARD; PRT; 132 AA.
 AC 077801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
 GN INSL3 OR RLF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97107158; PubMed=8949906;
 RA Bathgate R.A.D., Balvers M., Hunt N., Ivell R.;
 RT "Relaxin-like factor gene is highly expressed in the bovine ovary of
 the cycle and pregnancy: sequence and messenger ribonucleic acid
 analysis.";
 RL Biol. Reprod. 55:1452-1457(1996).
 CC -1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
 SPERMATOGENESIS.
 CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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CC or send an email to license@isb-sib.ch.
 CC EMBL: AF094580; AACG3380.1;
 DR InterPro: IPR000739; Insulin_IGF_relaxin.
 DR Pfam: PF00049; Insulin; 1.
 DR SMART: SM00078; ILGF; 1.
 DR PROSITE: PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 57 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
 FT PROPEP 59 104 C PEPTIDE (POTENTIAL).
 FT CHAIN 107 132 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
 FT DISULFID 34 117 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 46 130 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 116 121 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 14378 MW; A5585500C7F2241D CRC64;

Query Match 13.6%; Score 103.5; DB 1; Length 132;
 Best Local Similarity 28.5%; Pred. No. 0.0023;
 Matches 37; Conservative 17; Mismatches 43; Indels 33; Gaps 7;
 QY 23 AEARAAPYGVRLCGREFIRAVITCGGSRWRRSDILAHEAMGDTFPDADADS---LAG 79
 DB 24 AAQAEAP--EKLCGHFVRALVRLCGPRWSSE-----DGRVAGGDRLLRWLEG 73
 QY 80 E--LDEAMSGSSE---WLATKSPQA--FYGRPSWGTGVLGRGSRDVLGLSSCCCKWG 132
 DB 74 QHLLGLMAGSDPVLVLAQPLQASRHHHRRATAINP-----ARHCLSG 120
 QY 133 CSKSEISSIC 142
 DB 121 CTRODLTLIC 130

RESULT 11
 INL3_PIG STANDARD; PRT; 131 AA.
 AC P51461;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
 GN INSL3 OR RLF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94075362; PubMed=8253799;
 RA Adham I.M., Burkhardt E., Benahmed M., Engel W.;
 RT "Cloning of a cDNA for a novel insulin-like peptide of the testicular
 Leydig cells.";
 RL J. Biol. Chem. 268:26668-26672(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292172; PubMed=8020942;
 RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
 RA Engel W.;
 RT "Structural organization of the porcine and human genes coding for a
 Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
 localization of the human gene (INSL3).";
 RL Genomics 20:13-19(1994).
 CC -1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
 SPERMATOGENESIS.
 CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 DISULFIDE BONDS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND
 POSTNATAL LEYDIG CELLS.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

-I- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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| | | | | |
|------------|----------------------|----------------------|-----------------------------------------|--|
| | CC | | - - - - - | |
| EMBL: | AJ011961; | CRAO9888.1; | -- | |
| DR DR | EMBL; AJ011962; | CRAO9888.1; | JOINED. | |
| EMBL: | AJ011961; | CRAO9889.1; | -- | |
| HSSP: | P01315; | IzEI. | | |
| DR DR | InterPro; IPR000739; | Insulin_IGF_relatin. | | |
| DR DR | pfam; PF00049; | Insulin; 1. | | |
| SMART: | SM00078; | ILGF; 1. | | |
| PROSITE: | PS00262; | INSULIN; 1. | | |
| KW | Insulin family; | Hormone; Signal; | Alternative splicing. | |
| | SIGNAL: | 1 | POTENTIAL. | |
| FT CHAIN | 25 | 24 | L-LEU DGL INSULIN-LIKE PEPTIDE B CHAIN. | |
| FT PROPSEP | 58 | 55 | LYDYG INSULIN-LIKE PEPTIDE A CHAIN. | |
| FT CHAIN | 107 | 104 | INTERCHAIN (BY SIMILARITY). | |
| DISULFD | 34 | 131 | INTERCHAINS (BY SIMILARITY). | |
| DISULFD | 46 | 130 | | |

| FT | VARSPLOC | 64 | 74 | GEOLQWLEKRI | LEADING |
|----|----------|-----|-------|-----------------------------|-------------------------|
| FT | VARSPLOC | 64 | 74 | GEOLQWLEKRI | LEADING |
| FT | VARSPLOC | 75 | 131 | MISSING (IN SHORT ISOFORM). | ISOFORM). |
| FT | VARSPLOC | 131 | 14252 | MISSING | 685743CAEECF8731 CRC64; |

[illegible]

| | |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------|
| Oy | 142 C 142 |
| | |
| Db | 130 C 130 |
| | |
| RESULT 13 | |
| BELX_MACMU | |
| ID | STANDARD; PRT; 185 AA. |
| AC | P19884; |
| DT | 01-FEB-1991 (Rel. 17, Created) |
| DT | 01-FEB-1991 (Rel. 17, Last sequence update) |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) |
| DE | Prorelaxin precursor. |
| GN | RN. |
| OS | Macaca mulatta (Rhesus macaque). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; |
| OC | Cercopitheciinae; Macaca. |
| OX | NCBI_TaxID=9544; |
| RN | {1} |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=90073957; Pubmed=2590381; |
| RA | Crawford R.J., Hammond V.E., Roche P.J., Johnston P.D., Tregear G.W. ; |
| RT | "Structure of rhesus monkey relaxin predicted by analysis of the single-copy rhesus monkey relaxin gene."; |
| RL | J. Mol. Endocrinol. 3:169-174(1989). |
| CC | -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE |
| CC | INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY, |
| CC | |

PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR PIR; A34936; A34936.
 DR HSSP; P04090; 6RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 53 RELAXIN B CHAIN (PROBABLE).
 FT PROPEP 56 157 CONNECTING PEPTIDE (PROBABLE).
 FT CHAIN 161 185 RELAXIN A CHAIN (PROBABLE).
 FT DISULFID 35 172 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 47 185 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 171 176 BY SIMILARITY.
 SQ SEQUENCE 185 AA; 20895 MW; 7E3C5D21B57E185C CRC64;

Query Match 13.4%; Score 101.5; DB 1; Length 185;
 Best Local Similarity 22.7%; Pred. No. 0.0051;
 Matches 42; Conservative 22; Mismatches 78; Indels 43; Gaps 4;

QY 1 MARYMLLLIAVWVLGELWPGAEARAAPYGVRLCGREFIRAVFTCGGSRWRSDILAH 60
 Db 1 MPRLEFLHLLGCLLNQFSAVAKWMDVVKACGRELVAQIAICGKSTLGKRSLNQE 60
 QY 61 EAMDTFFPDADDESLAGELDEAMGSEWLA-----LTKSP----- 97
 Db 61 DAPLKPRAAEIVPSLIQDITETINMSEFVANLPQLKLTLSERQALSELQOHVPVLK 120
 QY 98 -----QAFYGRPS--WGTPGVLRG-----SRDLVAGLSGCCCKWGCKSKSE 137
 Db 121 DSNLSFEFKIIRKQSEATSSPSSELKSLGLDTHSRKRYLTWLSNKKCHIGCTKRS 180
 QY 138 ISSLC 142
 Db 181 LAKFC 185

RESULT 14
 ID RELX_RAJER STANDARD; PRT; 64 AA.
 AC P11952;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Relaxin.
 OS Raja erinacea (Little skate).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hymnosquales; Pristiorajae; Batoidae;
 OC Rajiformes; Rajidae; Raja.
 OX NCBI_Taxid=7782;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Ovary;
 RX MEDLINE=87156758; PubMed=3827922;
 RA Bullebach E.E., Schwabe C., Callard I.P.;
 RT "Relaxin from an oviparous species, the skate (Raja erinacea).";
 RL Biochem. Biophys. Res. Commun. 143:273-280(1987).
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR PIR; A29543; A29543.
 DR HSSP; P04090; 6RLX.
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.

Insulin family; Hormone.
 KW CHAIN 1 40 RELAXIN B CHAIN.
 FT NON_CONS 40 41
 FT CHAIN 41 64 RELAXIN A CHAIN.
 FT DISULFID 11 51 INTERCHAIN.
 FT DISULFID 23 64
 FT DISULFID 50 55
 SQ SEQUENCE 64 AA; 7499 MW; E7AC62B8BA81F49D CRC64;
 Query Match 13.2%; Score 100.5; DB 1; Length 64;
 Best Local Similarity 22.1%; Pred. No. 0.002;
 Matches 27; Conservative 11; Mismatches 25; Indels 59; Gaps 3;
 QY 21 PGAEARAAPYGVRLCGREFIRAVFTCGGSRWRSDILAHAMGDTTPDADADESLAGE 80
 Db 2 PNWEERS-----RLCGRLIRAFIYLCGTRWTLNPNFGNYP----- 39
 QY 81 LDEAMGSEWLAATKSPQAFYGRPSWGTPGVLRGSRDLVAGLSGCCCKWGCKSKSEISS 140
 Db 40 MEKMN-----GPAKKCCAIGCSTEDFRM 62
 QY 141 LC 142
 Db 63 VC 64

RESULT 15
 ID INL3_RAT STANDARD; PRT; 105 AA.
 AC Q9WUK0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor) (Fragment).
 DE INSL3 OR RLF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Spiess A.-N., Pusch W., Ivell R.;
 RT "Cloning and sequence of the rat relaxin-like factor and its promotor."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
 CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC DISULFIDE BONDS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 CC [1]
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; AF139918; AAD33663.1;
 DR InterPro; IPR000739; Insulin_IGF_relaxin.
 DR Pfam; PF00049; Insulin; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Insulin family; Hormone.
 FT NON_TER 1 1
 FT CHAIN <1 ?
 FT PROPEP ? 77
 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
 C PEPTIDE (POTENTIAL).

```

FT CHAIN      80 105 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFID   6 90 INTERCHAIN (BY SIMILARITY).
FT DISULFID  18 103 INTERCHAIN (BY SIMILARITY).
FT DISULFID  89 94 BY SIMILARITY.
SQ SEQUENCE 105 AA; 11674 MW; 903716A8FBEB13EE CRC64;

Query Match      13.2%; Score 100.5; DB 1; Length 105;
Best Local Similarity 24.8%; Pred. No. 0.0035;
Matches 35; Conservative 11; Mismatches 34; Indels 61; Gaps 6;

QY 25 ARAAPYGVRLCGREFIRAVITCGGSRWRRSDILAHEAMGDTFPDADADESLAGELDEA 84
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 ARA-----KLCGHLVRLVRCGGPRWS-----PEATQPVDTDRDEL--- 38

QY 85 MGSSEWL-----ALTKSP-----QAFYGRGRPSWOGTPGVLRGSRDVL 121
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 39 ---LQWLEQRHLHLVADADPALDPDPALDPQLPHQASQOR-----RSVA 82

QY 122 AGLSSCCCKWGCCKSEISLC 142
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 83 TNAVHRCCLTGCTQDQLGLC 103

```

Search completed: June 27, 2002, 16:16:51
Job time: 485 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:09 ; Search time 73.16 Seconds
(without alignments)
36.438 Million cell updates/sec

Title: US-09-781-077-2_COPY_119_142
Perfect score: 132
Sequence: 1 DVLGLSSCKWGCKSKSEISLC 24
Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_032802.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------|
| 1 | 132 | 100.0 | 142 | 22 | AA1980.DAT.* |
| 2 | 63 | 47.7 | 135 | 19 | AA1981.DAT.* |
| 3 | 63 | 47.7 | 135 | 21 | AA1982.DAT.* |
| 4 | 61 | 46.2 | 213 | 18 | AA1983.DAT.* |
| 5 | 61 | 46.2 | 213 | 19 | AA1984.DAT.* |
| 6 | 59 | 44.7 | 188 | 19 | AA1985.DAT.* |
| 7 | 58 | 43.9 | 22 | 4 | AA1986.DAT.* |
| 8 | 58 | 43.9 | 182 | 4 | AA1987.DAT.* |
| 9 | 58 | 43.9 | 182 | 5 | AA1988.DAT.* |
| 10 | 57 | 43.2 | 27 | 20 | AA1989.DAT.* |
| 11 | 57 | 43.2 | 135 | 19 | AA1990.DAT.* |

| | | | | | |
|----|------|------|------|----|--------------|
| 12 | 57 | 43.2 | 135 | 20 | AA1991.DAT.* |
| 13 | 57 | 43.2 | 135 | 21 | AA1992.DAT.* |
| 14 | 57 | 43.2 | 135 | 21 | AA1993.DAT.* |
| 15 | 57 | 43.2 | 135 | 21 | AA1994.DAT.* |
| 16 | 57 | 43.2 | 135 | 21 | AA1995.DAT.* |
| 17 | 57 | 43.2 | 135 | 22 | AA1996.DAT.* |
| 18 | 57 | 43.2 | 135 | 22 | AA1997.DAT.* |
| 19 | 57 | 43.2 | 135 | 22 | AA1998.DAT.* |
| 20 | 57 | 43.2 | 135 | 22 | AA1999.DAT.* |
| 21 | 57 | 43.2 | 135 | 22 | AA2000.DAT.* |
| 22 | 57 | 43.2 | 135 | 22 | AA2001.DAT.* |
| 23 | 56 | 42.4 | 1005 | 20 | AA1980.DAT.* |
| 24 | 55 | 41.7 | 877 | 19 | AA1981.DAT.* |
| 25 | 54 | 40.9 | 24 | 16 | AA1982.DAT.* |
| 26 | 53.5 | 40.5 | 162 | 22 | AA1983.DAT.* |
| 27 | 52 | 39.4 | 24 | 16 | AA1984.DAT.* |
| 28 | 52 | 39.4 | 24 | 18 | AA1985.DAT.* |
| 29 | 52 | 39.4 | 46 | 21 | AA1986.DAT.* |
| 30 | 52 | 39.4 | 150 | 16 | AA1987.DAT.* |
| 31 | 52 | 39.4 | 162 | 11 | AA1988.DAT.* |
| 32 | 52 | 39.4 | 164 | 11 | AA1989.DAT.* |
| 33 | 52 | 39.4 | 185 | 5 | AA1990.DAT.* |
| 34 | 52 | 39.4 | 185 | 10 | AA1991.DAT.* |
| 35 | 51.5 | 39.0 | 133 | 22 | AA1992.DAT.* |
| 36 | 51.5 | 39.0 | 888 | 22 | AA1993.DAT.* |
| 37 | 51 | 38.6 | 93 | 22 | AA1994.DAT.* |
| 38 | 51 | 38.6 | 313 | 21 | AA1995.DAT.* |
| 39 | 51 | 38.6 | 313 | 21 | AA1996.DAT.* |
| 40 | 51 | 38.6 | 313 | 21 | AA1997.DAT.* |
| 41 | 51 | 38.6 | 313 | 21 | AA1998.DAT.* |
| 42 | 51 | 38.6 | 325 | 21 | AA1999.DAT.* |
| 43 | 51 | 38.6 | 325 | 21 | AA2000.DAT.* |
| 44 | 51 | 38.6 | 325 | 21 | AA2001.DAT.* |
| 45 | 51 | 38.6 | 325 | 21 | AA2002.DAT.* |

ALIGNMENTS

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|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 100.0%; | Score 132; | DB 22; | Length 142; |
| Best Local Similarity | 100.0%; | Pred. No. 1.5e-09; | | |
| Matches 24: | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

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|--------------------------|-------|----------------|-----------|------------|
| Query Match | 47.7% | Score 63 | DB 19 | Length 135 |
| Best Local Similarity | 52.6% | Pred. No. 0.88 | | |
| Matches 10; Conservative | 4; | Mismatches 5; | Indels 0; | Gaps 0; |

QY 6 LSSCCKWGCSKSEISSL 24
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Db 117 lqalcrcgcmkclstlc 135

RESULT 3

AA95771
ID AAY95771 standard; Protein; 135 AA.

AC AAY95771;

XX
DT 07-NOV-2000 (first entry)

XX Mouse insulin family homologue zins3.

XX Zins3; insulin; relaxin; mouse; NIDDM;
KW non-insulin dependent diabetes mellitus; diagnosis.

XX Mus musculus.

XX WO200047776-A2.

PN 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03515.

XX 12-FEB-1999; 99US-0198248.

PR 12-FEB-1999; 99US-0250125.

XX (ZYMO) ZYMOGENETICS INC.

PA Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;

PI WPI; 2000-558220/51.

DR N-PSDB; AAA50153.

XX Identifying mutations in human chromosome 1p31, preferably a zins3 gene
PT mutation, comprises using an insulin/relaxin family member (designated
PT zins3), useful for diagnosing non-insulin dependent diabetes

XX Example 4; Page 46-47; 51pp; English.

CC The present sequence is that of a murine paralog (see AAY95771) of
CC human zins3 (see AAY95770), a novel member of the insulin/relaxin
CC family member that maps to a region of human chromosome 1 associated
CC with non-insulin dependent diabetes mellitus (NIDDM). The sequence
CC was deduced from an isolated cDNA clone (see AAA50153). Northern
CC blots of embryo tissue indicated that mouse zins3 is expressed in
CC a developmentally regulated fashion. zins3 polynucleotides and
CC polypeptides can be used to diagnose disorders associated with
CC abnormal expression of zins3, and to identify polymorphisms that
CC result from mutations in the human zins3 gene. The invention
CC provides methods for identifying abnormalities in expression that
CC are a factor in causing, or predisposing, a person to some defect
CC in glucose metabolism, such as NIDDM.

XX Sequence 135 AA;

Query Match

Best Local Similarity 47.7%; Score 63; DB 21; Length 135;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCKKWCCKSKSEISL 24

DB 117 lqalcrcgcmkclstlc 135

RESULT 4

AAW17675
ID AAW17675 standard; Protein; 213 AA.

AC AAW17675;

XX 24-JUL-1997 (first entry)

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FT

Human relaxin-related factor-1 (RRF-1).

Relaxin-related factor-1; RRF-1; testis; sperm; growth factor;
infertility.

Homo sapiens.

Key

Peptide

Location/Qualifiers

1-29

/label- Sig_peptide

Misc-difference 178

/note=

"conserved Cys residue indicative of

insulin family member"

Misc-difference 179

/note=

"conserved Cys residue indicative of

insulin family member"

Misc-difference 183

/note=

"conserved Cys residue indicative of

insulin family member"

Misc-difference 192

/note=

"conserved Cys residue indicative of

insulin family member"

WO9716549-A2.

09-MAY-1997.

01-NOV-1996; 96WO-US17342.

21-FEB-1996; 96US-0012016.

03-NOV-1995; 95US-0006221.

(REGE-) REGENERON PHARM INC.

Davis S;

WPI; 1997-272118/24.

N-PSDB; AAT68418.

New isolated relaxin-related factor genes - used to develop products
PT which can be used in diagnosis and therapy, e.g. in fertility and
PT pregnancy applications

XX Example 1; Fig 1; 34pp; English.

XX Human relaxin-related factor-1 (RRF-1) (AAW17675) is a testis-

CC specific growth factor related to relaxin and to the insulin family

CC of ligands. RRF-1 cDNA (AAT68418) was isolated in a search of

CC expressed sequence tags for sequences related to relaxin. RRF-1

CC displays all the expected features of a new insulin family member,

CC partic. with regard to a cluster of four cysteine residues at the

CC C-terminus of the molecule. A related placenta-specific factor,

CC RRF-2 (AAW17676), has also been identified. RRF-1 can be produced

CC in transfected host cells for use in the prepn. of antibodies and

CC therapeutic compns., or as a growth factor for maintaining cells

CC in culture. RRF-1 may be involved in the maturation of sperm and

CC may have a role in treatment of fertility disorders.

XX Sequence 213 AA;

Query Match

Best Local Similarity 46.2%; Score 61; DB 18; Length 213;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCKKWCCKSKSEISL 24

DB 173 gysekcccltgcckeeIsiac 192

RESULT 5

AAW47548

us-09-781-077-2_copy_119_142.rag

Fri Jun 28 11:32:03 2002

XX Rattus rattus.
 XX OS
 XX WO9805782-A1.
 XX PN
 XX 12-FEB-1998.
 XX PD
 XX 01-AUG-1997; 97WO-US13879.
 XX PF
 XX 21-NOV-1996; 96US-0031592.
 XX PR
 XX 02-AUG-1996; 96US-0023213.
 XX PA
 XX (ZYMO) ZYMOGENETICS INC.
 XX PI
 XX Adams RL, Conklin DC, Jaspers SR, Jelmborg AC, Lofton-Day CE;
 XX PI Lok S;
 XX DR
 XX WPI; 1998-145618/13.
 XX DR N-PSDB; AAV18662.
 XX XX
 XX Testis-specific insulin homologue poly:peptide(s) - may be used,
 XX PT e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm
 XX PT motility or in immuno:contraception methods
 XX PS
 XX Claim 8; Pages 66-67; 91pp; English.
 XX XX
 XX The present sequence is rat Zins2 testis-specific insulin
 XX CC homologue, which may be used to enhance the viability of
 XX CC cryopreserved sperm, sperm motility, egg/sperm interactions,
 XX CC fertilisation or proliferation or differentiation of testicular
 XX CC cells. Zins2 may also be used as a vaccine, e.g. in
 XX CC immunocontraception methods to prevent fertilisation. Antagonists,
 XX CC e.g. anti-zins2 binding protein, may be used in contraception.
 XX CC Zins2 is especially useful for in vitro fertilisation methods.
 XX SQ
 XX Sequence 188 AA;

Query Match 44.7%; Score 59; DB 19; Length 188;
 Best Local Similarity 45.0%; Pred. No. 3.8;
 Matches 9; Conservative

QY 5 GLSSSCCKWGCKSEISLSC 24
 | : || |||| | : |
 Db 163 gfadkccaigcskeelavac 182

RESULT 7
 AAP30192
 ID AAP30192 standard; Protein; 22 AA.
 XX AC
 XX AAP30192;
 XX DT 03-AUG-1992 (first entry)
 XX XX
 XX Sequence encoded by synthetic gene for porcine relaxin A chain.
 XX DE Hormone; labour; pregnancy; parturition; control; induction.
 XX KW Pig.
 XX OS
 XX EP68375-A.
 XX PN
 XX 05-JAN-1983.
 XX PD
 XX 19-JUN-1982; 82EP-0105405.
 XX PF
 XX 22-JUN-1981; 81GB-0019138.
 XX PR
 XX (SEAR) SEARLE G D & CO.
 XX PA
 XX Stewart AG, Bell LD;
 XX PI
 XX

AAW47548 standard; Protein; 213 AA.
 AC
 AAW47548;
 03-JUL-1998 (first entry)
 Human zins2 testis-specific insulin homologue.
 Human; zins2; testis-specific insulin homologue; differentiation;
 cryopreserved sperm viability; sperm motility; proliferation;
 egg/sperm interaction; fertilisation; testicular cell; vaccine;
 immunocontraception; contraception; in vitro fertilisation.
 Homo sapiens.
 WO9805782-A1.
 12-FEB-1998.
 01-AUG-1997; 97WO-US13879.
 21-NOV-1996; 96US-0031592.
 02-AUG-1996; 96US-0023213.
 (ZYMO) ZYMOGENETICS INC.
 Adams RL, Conklin DC, Jaspers SR, Jelmborg AC, Lofton-Day CE;
 Lok S;
 WPI; 1998-145618/13.
 N-PSDB; AAV18663.
 Testis-specific insulin homologue poly:peptide(s) - may be used,
 e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm
 motility or in immuno:contraception methods
 Claim 10; Pages 73-74; 91pp; English.
 The present sequence is human Zins2 testis-specific insulin
 homologue, which may be used to enhance the viability of
 cryopreserved sperm, sperm motility, egg/sperm interactions,
 fertilisation or proliferation or differentiation of testicular
 cells. Zins2 may also be used as a vaccine, e.g. in
 immunocontraception methods to prevent fertilisation. Antagonists,
 e.g. anti-zins2 binding protein, may be used in contraception.
 Zins2 is especially useful for in vitro fertilisation methods.

Query Match 46.2%; Score 61; DB 19; Length 213;
 Best Local Similarity 50.0%; Pred. No. 2.4;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSSCCKWGCKSEISLSC 24
 | : || |||| | : |
 Db 173 gysekccitgtckeelsiac 192

RESULT 6
 AAW47547
 ID AAW47547 standard; Protein; 188 AA.
 XX AC
 XX AAW47547;
 XX DT 03-JUL-1998 (first entry)
 XX XX
 XX Rat zins2 testis-specific insulin homologue.
 XX DE Rat; zins2; testis-specific insulin homologue; differentiation;
 XX KW cryopreserved sperm viability; sperm motility; proliferation;
 KW egg/sperm interaction; fertilisation; testicular cell; vaccine;
 KW immunocontraception; contraception; in vitro fertilisation.

DR WPI; 1983-04897K/03.
XX N-PSDB; AAN30124.

PT Prodn. of porcine relaxin from synthetic genes - useful for
XX induction and control of labour in women
XX Disclosure; Fig 1; 38pp; English.

XX The inventors claim synthetic genes for porcine relaxin. The genes
CC may contain, in addn. to the coding sequence, a stop codon, an
CC initiator methionine codon, restriction sites for Cla I and Bam HI
CC etc. Porcine relaxin is useful in the induction and control of
CC labour in women. In sows admin. during farrowing may reduce the
CC rate of still birth of piglets.

XX Sequence 22 AA;

Query Match 43.9%; Score 58; DB 4; Length 22;
Best Local Similarity 47.4%; Pred. No. 0.74;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISSLC 24
DB 4 lsekccqvcirkdiaric 22

RESULT 8

AAP30392
ID AAP30392 standard; Protein; 182 AA.

XX AAP30392;

DT 25-MAY-1992 (first entry)

DE Sequence of porcine preprorelaxin.

XX Relaxin; hormone.

XX Sus scrofa domestica.

XX EP86649-A.

PD 24-AUG-1983.

PF 12-FEB-1983; 83EP-0021967.

PR 12-FEB-1982; 82AU-0002695.
PR 11-FEB-1983; 83AU-0011834.

XX (FLOR-) FLOREY INST EXP PHY.
PA (HOWA-) HOWARD FLOREY INST.

PI Hudson PJ, Haley JD, Niall HD, Shine J;

XX WPI; 1983-748587/35.
XX N-PSDB; AAN30196.

XX Genes and DNA transfer vectors for prorelaxin expression - useful
XX in prodn. of porcine relaxin for veterinary and human use

XX Disclosure; Fig 5; 50pp; English.

XX The inventors claim synthetic porcine preprorelaxin and prorelaxin
CC and synthetic A, B and C peptide chains of prolaxin, and a gene for
CC expression of porcine preprorelaxin or prorelaxin, and their sub-
CC units (see AAN30186). They also claim a double-stranded DNA fragment
CC for the expression of the signal peptide chain of porcine
CC preprorelaxin comprising a coding strand and a complementary strand
CC corresp. to a defined mRNA sequence (see AAN30187-N30194) which
CC corresp. to the most homologous regions between the pig and rat cDNA
CC sequences. A probe (AAN30195) is also claimed.

SQ Sequence 182 AA;

Query Match 43.9%; Score 58; DB 4; Length 182;
Best Local Similarity 47.4%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISSLC 24
DB 164 lsekccqvcirkdiaric 182

RESULT 9

AAP40156
ID AAP40156 standard; Protein; 182 AA.

XX AAP40156;

DT 11-FEB-1992 (first entry)

DE Sequence of porcine preprorelaxin.

XX Labour; birth; hormone; relaxin.

XX Fig.

XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= signal
FT Peptide 26..57
FT /label= B-chain
FT Peptide 58..160
FT /label= C-peptide
FT Peptide 161..182
FT /label= A-chain

XX EPI01309-A.

XX 22-FEB-1984.

XX 11-AUG-1983; 83EP-0304662.

XX 12-AUG-1982; 82AU-0005352.
XX 11-AUG-1983; 83AU-0017906.
XX 01-JAN-1988; 88EP-0104503.

XX (FLOR-) HOWARD FLOREY INST.
XX (HOWA-) HOWARD FLOREY INST.

XX Hudson PJ, Shine J, Niall HD, Tregear GW;

XX WPI; 1984-050918/09.
XX N-PSDB; AAN40125, AAN40126.

XX Genes for human relaxin, prorelaxin and preprorelaxin prodn. -
XX prepd. by recombinant DNA techniques

XX Disclosure; Fig 3; 51pp; English.

XX The inventors claim the gene for the expression of human
XX preprorelaxin (HPP) and its sub-units. Also claimed are synthetic
XX HPP, HP, fragments and analogues. Human relaxin and its analogues
XX are prepd. for therapeutic purposes, esp. in clinical intervention
XX in cases of difficult labour.

XX Sequence 182 AA;

Query Match 43.9%; Score 58; DB 5; Length 182;
Best Local Similarity 47.4%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCSEISSLC 24

Db 164 lsekccqvcirkdialc 182

RESULT 10

AAV01962
ID AAY01962 standard; Peptide; 27 AA.

XX AC AAY01962;

XX DT 01-JUL-1999 (first entry)

XX DE Insulin-like peptide (pro-ILP) chain A peptide.

XX KW Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;

XX KW A chain; B chain; C chain; neurophysiological function;

XX KW fluid homeostasis; electrolyte homeostasis; cardiovascular function;

XX KW blood pressure; somatic; cardiac ionotropic activity;

XX KW cardiac chronotropic activity; collagen deposition.

XX OS Homo sapiens.

XX PN WO9915664-A1.

XX PD 01-APR-1999.

XX PF 28-AUG-1998; 98WO-US17888.

XX PR 24-SEP-1997; 97US-0059836.

XX PA (GETH) GENENTECH INC.

XX PI Gurney A;

XX DR WPI; 1999-254713/21.

XX DR N-PSDB; AAX35209.

XX PT Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function

XX PS Claim 7; Page -: 75pp; English.

XX CC The present sequence represents insulin-like polypeptide (pro-ILP) chain A peptide. The ILP protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises an A chain and a B chain linked by disulfide bonds. The C-peptide of pro-ILP exists as a separate peptide after processing of pro-ILP. The ILP protein is useful in treatment of disorders related to neurophysiological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac ionotropic activity, cardiac chronotropic activity and collagen deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and screening of modulators and therapeutics. note: the present sequence does not appear in the specification; it was created using information provided.

XX SQ Sequence 27 AA;

Query Match 43.2%; Score 57; DB 20; Length 27;

Best Local Similarity 47.4%; Pred. No. 1.2;

Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISL 24

DB 9 lqtlcctdgcsmtdsalc 27

RESULT 11

AAW37925

ID AAW37925 standard; Protein; 135 AA.

XX AC AAW37925;

XX DT 01-SEP-1998 (first entry)

XX DE Human Zins3 protein.

XX KW Insulin homologue; identification; isolation; Zins3 receptor; treatment; disease; pre-eclampsia; premature labour; Human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 23..48

XX FT Peptide /note= "B chain"

XX FT Peptide 49..114

XX FT Peptide /note= "C-peptide"

XX FT Peptide 115..135

XX FT Peptide /note= "A chain"

XX PN WO9816635-A1.

XX PD 23-APR-1998.

XX PF 15-OCT-1997; 97WO-US18593.

XX PR 15-OCT-1996; 96US-0028177.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;

XX DR WPI; 1998-251285/22.

XX DR N-PSDB; AAV29150.

XX PT Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease

XX PS Claim 2; Page 64-65; 81pp; English.

XX CC The Zins3 protein is an insulin homologue protein. Polynucleotide molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a nonhuman animal. The polypeptides can be used to identify and isolate receptors for Zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases associated with the polypeptide, such as reproductive disorders associated with the placenta and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as pre-eclampsia, premature labour, and Crohn's disease.

XX SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 19; Length 135;

Best Local Similarity 47.4%; Pred. No. 5.1;

Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISL 24

DB 117 lqtlcctdgcsmtdsalc 135

RESULT 12

AAV01961

ID AAY01961 standard; Protein; 135 AA.

XX AC AAY01961;

XX XX

CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.

XX
SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LSSSCCKWGCSEISLSC 24
| : || ||| :|||
Db 117 lqtclctdgcsmtdlsalc 135

RESULT 15
AAY95770
ID AAY95770 standard; Protein; 135 AA.
XX AC AAY95770;
XX DT 07-NOV-2000 (first entry)
XX DE Human insulin family homologue zins3.
XX KW Zins3; insulin; relaxin; human; diagnosis; NIIDM;
XX KW non-insulin dependent diabetes mellitus.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Peptide 23..48 /label= B-chain
FT Peptide 49..114 /label= C-chain
FT Peptide 115..135 /label= A-chain
XX WO200047776-A2.
XX PN 17-AUG-2000.
XX PD 10-FEB-2000; 2000WO-US03515.
XX PF 12-FEB-1999; 99US-0198248.
XX PR 12-FEB-1999; 99US-0250125.
XX XX (ZYMO) ZYMOGENETICS INC.
XX PI Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
XX WPI: 2000-558220/51.
XX N-PSDB; AAA50150.
XX DR Identifying mutations in human chromosome 1p31, preferably a zins3 gene
XX PT mutation, comprises using an insulin/relaxin family member (designated
XX PT zins3), useful for diagnosing non-insulin dependent diabetes -
XX PS Claim 2; Page 44-45; 51pp; English.
XX CC The present sequence is that of zins3, a novel member of the
XX CC insulin/relaxin family. The zins3 gene maps to human chromosome
XX CC 1p31, a region that is correlated to a heritable form of non-insulin
XX CC dependent diabetes mellitus (NIIDM). zins3 mRNA is not expressed

Qy 6 LSSSCCKWGCSEISLSC 24
| : || ||| :|||
Db 117 lqtclctdgcsmtdlsalc 135

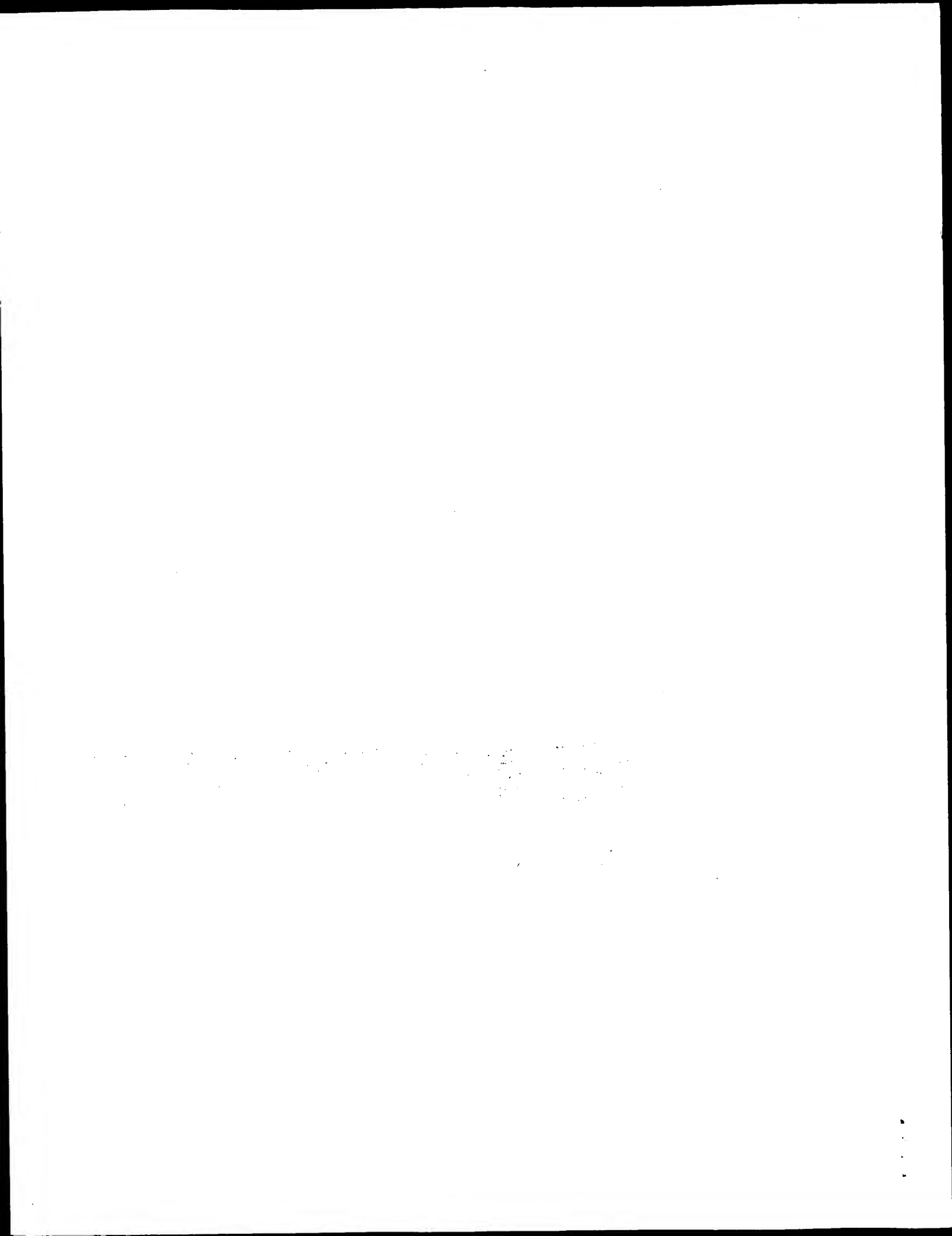
RESULT 14
AAB24391
ID AAB24391 standard; Protein; 135 AA.
XX AC AAB24391;
XX DT 07-NOV-2000 (first entry)
XX DE Human PRO182 protein sequence SEQ ID NO:16.
XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
XX KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
XX KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
XX KW cytostatic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO200032221-A2.
XX PD 08-JUN-2000.
XX PF 30-NOV-1999; 99WO-US28313.
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 16-DEC-1998; 98US-0112850.
XX PR 12-JAN-1999; 99US-0115554.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 28-APR-1999; 99US-0131445.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 05-OCT-1999; 99WO-US21547.
XX PR 29-OCT-1999; 99US-0162506.
XX XX (GETH) GENENTECH INC.
XX PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
XX PI Watanabe CK, Williams PM, Wood WI;
XX XX WPI: 2000-412154/35.
XX DR N-PSDB; AAA77521.
XX PT Nucleic acids encoding PRO polypeptides useful for preventing,
XX PT diagnosing and treating diabetes a cardiovascular, endothelial or
XX PT angiogenic disorders in mammals -
XX XX Claim 72; Fig 8; 315pp; English.
XX CC The present invention describes nucleic acids encoding PRO polypeptides
XX CC useful for preventing, diagnosing and treating diabetes a
XX CC cardiovascular, endothelial or angiogenic disorder in mammals by
XX CC modulating cell proliferation, angiogenesis and cardiovascularisation,
XX CC and for identifying agonists and antagonists of these processes. The

CC in detectable amounts in healthy tissue, indicating that the zins3
CC polynucleotide is a candidate marker for a disease state and/or a
CC specialized cell type. zins3 polynucleotides and polypeptides can
CC be used to diagnose disorders associated with abnormal expression
CC of the zins3 protein, and to identify polymorphisms that result
CC from mutations in the zins3 gene. In particular, the invention
CC provides methods for identifying abnormalities in expression that
CC are a factor in causing, or predisposing, a person to some defect
CC in glucose metabolism, such as NIDDM. Processing of the mature
CC zins3 protein involves cleavage at the C-terminus of the signal
CC peptide and, based on predicted structural homology with other
CC members of the insulin family, cleavage at the C-terminus of the
CC B-chain and at the N-terminus of the A-chain, resulting in
CC removal of the C-peptide. Cysteine residues at positions 29 and 41
CC (B-chain) and 121 and 135 (A-chain) are capable of associating
CC through cysteine bridges and forming disulfide-bonded molecules.
XX
SQ Sequence 135 AA;

Query Match 43.2%; Score 57; DB 21; Length 135;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSCKKGGCKSKSEISLSC 24
| : || ||| : : |||
Db 117 lqtldctdgcsmtdlsalc 135

Search completed: June 27, 2002, 16:08:09
Job time: 278 sec



QY 6 LSSCCCKGCKSKSEISL 24
: | | | | | : | | | |
Db 6 MSIKCCIYGCTKKDISVLC 24

RESULT 3
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,267
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-905-267-13

Query Match 46.2%; Score 61; DB 2; Length 213;
Best Local Similarity 50.0%; Pred. No. 0.43;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCCCKGCKSKSEISL 24
: | | | | | : | | | | |
Db 173 GYSEKCLTGCTKEELSIAC 192

RESULT 5
US-09-314-051-13
; Sequence 13, Application US/09314051
; Patent No. 6183991
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,051
; FILING DATE:

QY 6 LSSCCCKGCKSKSEISL 24
: | | | | | : | | | |
Db 6 MSIKCCIYGCTKKDISVLC 24

RESULT 4
US-08-905-267-13
; Sequence 13, Application US/08905267
; Patent No. 5959075
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Jelmsberg, Anna C.

Query Match 47.7%; Score 63; DB 3; Length 135;
Best Local Similarity 52.6%; Pred. No. 0.15;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSCCCKGCKSKSEISL 24
: | | | | | : | | | |
Db 117 LQALCCRCGCKMKELSTLC 135

RESULT 3
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-950-720A-6

| | | | | |
|-----------------------|-------|----------------|-------|-------------|
| Query Match | 44.7% | Score 59; | DB 2; | Length 188; |
| Best Local Similarity | 45.0% | Pred. No. 0.7; | | |

| | | | | |
|-----------------------|-----------------|----------------|----------|-------------|
| Query Match | 44.7% | Score 59; | DB 4; | Length 188; |
| Best Local Similarity | 45.0% | Pred. No. 0.7; | | |
| Matches | 9: Conservative | 3: Mismatch | 8: Indel | |

; APPLICANT: HENNER, DENNIS J.; VANDIEN, RICHARD L.; WILKINS,
 ; JAMES A.; YANSURA, DANIEL G.
 ; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
 ; ISOLATION HUMAN RELAXIN
 ; NUMBER OF SEQUENCES: 42
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/908,766
 ; FILING DATE: 01-JUL-1992

```

RESULT 10
US-08-950-720A-2
; Sequence 2, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

RESULT 11
US-08-442-248-2
: Sequence 2, Application US/08442248
: Patent No. 5759863
: GENERAL INFORMATION:
: APPLICANT: Caras, Ingrid W.
: APPLICANT: Winslow, John W.
: TITLE OF INVENTION: AL-1 Neurotrophic Factor
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,248
: FILING DATE: 15-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/330128
: FILING DATE: 27-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: 920C4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-8674
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 928 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-442-248-2

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Query Match 43.2%; Score 57; DB 1; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 12

US-08-440-815-2
 ; Sequence 2, Application US/08440815
 ; Patent No. 5798448
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Winslow, John W.
 ; TITLE OF INVENTION: AL-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,815
 FILING DATE: 15-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/330128
 FILING DATE: 27-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: 920C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 928 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-440-815-2

Query Match 43.2%; Score 57; DB 1; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 13

US-08-486-449-2
 ; Sequence 2, Application US/08486449
 ; Patent No. 6280732
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Winslow, John W.
 ; TITLE OF INVENTION: AL-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,449
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/330128
 FILING DATE: 27-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: P0920P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 928 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-486-449-2

Query Match 43.2%; Score 57; DB 4; Length 928;
 Best Local Similarity 57.9%; Pred. No. 5.8;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCSEISSLC 24
 |||||: ||: |||||
 Db 485 LSGSCCEGCGRA--SSLC 501

RESULT 14

US-08-469-537A-103
 ; Sequence 103, Application US/08469537A
 ; Patent No. 5843749
 ; GENERAL INFORMATION:
 ; APPLICANT: Maisonnier, et al.
 ; TITLE OF INVENTION: EHK AND ROR TYROSINE
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: Tarrytown
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10591
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/469,537A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/406,247
 ; FILING DATE: 17-MAR-1995
 ; APPLICATION NUMBER: USSN 08/144,992
 ; FILING DATE: 28-OCT-1993
 ; APPLICATION NUMBER: USSN 07/736,559

Fri Jun 28 11:32:03 2002

;; FILING DATE: 26-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kempler, Ph.D., Gail M
;; REGISTRATION NUMBER: 32,143
;; REFERENCE/DOCKET NUMBER: REG 070C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 914-345-7400
;; TELEFAX: 914-345-7721
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1005 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-469-537A-103

Query Match 43.2%; Score 57; DB 2; Length 1005;
Best Local Similarity 57.9%; Pred. No. 6.3;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSCCCKWGCSEISLSC 24
|||: ||: |||
Db 596 LSGCCCGCGGRA--SSLSC 612

RESULT 15
5464756-1
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; VANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO: 1:
; LENGTH: 24
5464756-1

Query Match 42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSCCCKWGCSEISLSC 24
||: ||: ||: ||: ||: ||
Db 6 LSNKCHIGCTKKSLAKFC 24

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:09:27 ; Search time 36.01 Seconds
(without alignments)
64.042 Million cell updates/sec

Title: US-09-781-077-2_COPY_119_142

Perfect score: 132

Sequence: 1 DVLGLSSCKWGCKSEISILC 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|--------|---------------------|
| 1 | 74 | 56.1 | 54 | 2 | A26463 | relaxin - spiny do |
| 2 | 66 | 50.0 | 48 | 2 | A49739 | relaxin - horse (f |
| 3 | 63 | 47.7 | 44 | 1 | RXRKOT | relaxin - sand tig |
| 4 | 58 | 43.9 | 22 | 2 | B58793 | relaxin chain A - |
| 5 | 58 | 43.9 | 54 | 2 | A32201 | relaxin - Bryde's |
| 6 | 58 | 43.9 | 54 | 2 | B32201 | relaxin - minke wh |
| 7 | 58 | 43.9 | 182 | 1 | RAPG | relaxin precursor |
| 8 | 57 | 43.2 | 59 | 2 | A53879 | relaxin - dog (fra |
| 9 | 57 | 43.2 | 186 | 1 | RXRT | relaxin precursor |
| 10 | 57 | 43.2 | 893 | 2 | S51603 | receptor-like tyro |
| 11 | 57 | 43.2 | 898 | 2 | S47489 | receptor tyrosine |
| 12 | 57 | 43.2 | 1005 | 2 | S49015 | relaxin - baboon (|
| 13 | 56 | 42.4 | 24 | 2 | S42776 | relaxin homolog ce |
| 14 | 56 | 42.4 | 91 | 2 | T37327 | relaxin precursor |
| 15 | 56 | 42.4 | 185 | 2 | A34936 | brain-specific kin |
| 16 | 55 | 41.7 | 877 | 2 | I48967 | relaxin - oranguta |
| 17 | 53 | 40.2 | 221 | 2 | S07756 | relaxin - gorilla |
| 18 | 52 | 39.4 | 24 | 2 | S42780 | insulin-related pr |
| 19 | 52 | 39.4 | 57 | 2 | S42784 | relaxin 2 precursor |
| 20 | 52 | 39.4 | 145 | 2 | S43224 | relaxin 2 precursor |
| 21 | 52 | 39.4 | 166 | 2 | S42786 | hypothetical prote |
| 22 | 52 | 39.4 | 185 | 1 | A60982 | probable two-compo |
| 23 | 51 | 38.6 | 63 | 2 | S00951 | relaxin B,C and A |
| 24 | 51 | 38.6 | 1159 | 2 | E83237 | hypothetical prote |
| 25 | 50 | 37.9 | 143 | 2 | I47053 | hypothetical prote |
| 26 | 50 | 37.9 | 399 | 2 | T21586 | endo-1,4-beta-mann |
| 27 | 50 | 37.9 | 823 | 2 | T34472 | relaxin - little s |
| 28 | 49.5 | 37.5 | 448 | 2 | T48214 | |
| 29 | 49 | 37.1 | 64 | 2 | A29543 | |

30 49 37.1 169 1 S18946 ultra high-sulfur
31 49 37.1 185 2 S48082 relaxin precursor
32 49 37.1 2871 2 A55824 fibrillin-1 precur
33 48 36.4 60 2 S31723 metallothionein -
34 48 36.4 160 2 A49194 relaxin - guinea p
35 48 36.4 332 2 T04851 hypothetical prote
36 48 36.4 444 2 T42979 hypothetical prote
37 48 36.4 2233 2 T28669 surface protein 51
38 47 35.6 50 1 IWT02 insulin 2 - toadfi
39 47 35.6 51 2 S63590 insulin - duckbill
40 47 35.6 60 2 S38335 metallothionein -
41 47 35.6 99 2 JQ0902 bombaxin A-1 homol
42 47 35.6 108 2 S43582 insulin homolog 2
43 47 35.6 118 2 S52549 thionin variant Th
44 47 35.6 131 2 A53024 leydig insulin-lik
45 47 35.6 136 2 S52545 thionin variant Th

ALIGNMENTS

RESULT 1

A26463

relaxin - spiny dogfish (fragments)

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 19-Nov-1988 #sequence_revision 26-May-1995 #text_change 26-May-1995

C:Accession: B26463; A26463

R:Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.

Eur. J. Biochem. 161, 335-341, 1986

A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squ

A:Reference number: A91179; MUID:87054035

A:Accession: B26463

A:Molecule type: protein

A:Residues: 'E',2-30 <BUL>

A:Experimental source: ovary

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h

A:Accession: A26463

A:Molecule type: protein

A:Residues: 31-54 <BU2>

A:Experimental source: ovary

C:Superfamily: insulin

C:Keywords: hormone; pyroglutamic acid

F:1-30,31-54/Product: relaxin #status experimental <MAT>

F:1-30/Domain: chain B #status experimental <CHA>

F:31-54/Domain: chain A #status experimental <CHA>

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:13-41,25-54,40-45/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 56.1%; Score 74; DB 2; Length 54;

Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 GLSSSCCKWGCKSEISILC 24

Db 35 GMSKCKCTGCTRKDISILC 54

RELAXIN - horse (fragments)

A49739

C:Species: Equus caballus (domestic horse)

C:Date: 07-Apr-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995

C:Accession: B49739; A49739

R:Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R.

Endocrinology 129, 375-383, 1991

A:Title: Affinity purification and sequence determination of equine relaxin.

A:Reference number: A49739; MUID:91275796

A:Accession: B49739

A:Molecule type: protein

A:Residues: 1-28 <STE>

A:Accession: A49739

A:Molecule type: protein


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Query Match          43.9%;      Score 58; DB 1;      Length 182;
Best Local Similarity 47.4%;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      6  LSSCCCKWGCSEISLSC 24
      || || : || : ||
Db      164 LSEKCCQVCGRKDIARLC 182

RESULT 8

```

A: residues: 1-186 <HVD>
 A:Cross-references: GB:J00780; GB:M25468; NID:g206606; PIDN:AAAA2029.1; PID:
 C:superfamily: insulin
 C:keywords: hormone; ovary; pyroglutamic acid
 F.F.1-22/Domain: signal sequence #status predicted <STG>
 F.F.23-57/Domain: relaxin chain B #status predicted <RXB>
 F.F.58-163/Domain: relaxin #status predicted <MAT>
 F.F.163/Domain: relaxin connecting C peptide #status predicted <RXC>
 F.F.163/Domain: relaxin chain A #status predicted <RAX>
 F.F.36-173/48-186,172-177/Disulfide bonds: #status predicted <RAX>
 F.F.163/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #sta

```

Query Match      43.2%;   Score 57;   DB 1;   Length 186;
Best Local Similarity 47.4%;   Pred. No. 1.3;
Matches 9;   Conservative 3;   Mismatches 7;   Indels 0;   Gaps
                                0
Dy      6  LSSCCCKWGCKSEISSLC 24
      ||  ||  ||  ||  ||  ||
Db      168  LSEQCCHIGCTRRSIAKLC 186

RESULT 10
351603
receptor-like tyrosine kinase Ehk-1 - rat

```

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
 A:Accession: S51603
 R:Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase family
 A:Reference number: S49015; MUID:9406777
 A:Accession: S51603
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-893 <MAI>
 A:Cross-references: EMBL:S68028
 A:Note: the authors translated the codon GAC for residue 170 as Glu
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:563-829/Domain: protein kinase homology <KIN>
 F:571-579/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 893;
 Best Local Similarity 57.9%; Pred. No. 4.6;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 484 LSGSCCEGCGRA--SSLC 500

RESULT 11
 S47489
 receptor tyrosine kinase - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
 C:Accession: S47489
 R:Taylor, V.; Pfaff, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassmann, H.; St
 submitted to the EMBL Data Library, April 1994
 A:Description: Expression and developmental regulation of Etk-1, a neuronal ELK-like rec
 A:Reference number: S47489
 A:Accession: S47489
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-898 <TAI>
 A:Cross-references: EMBL:X78689; NID:g531543; PIDN:CAA55357.1; PID:g531544
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; transmembrane protein
 F:568-834/Domain: protein kinase homology <KIN>
 F:576-584/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 898;
 Best Local Similarity 57.9%; Pred. No. 4.6;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 489 LSGSCCEGCGRA--SSLC 505

RESULT 12
 S49015
 receptor tyrosine kinase Etk-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
 A:Accession: S49015; S51602
 R:Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A:Reference number: S49015; MUID:9406777
 A:Accession: S49015
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1005 <MAI>
 A:Cross-references: EMBL:S68024

A:Note: the authors translated the codon GAC for residue 170 as Glu
 A:Accession: S51602
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-305, 'G', 359-1005 <MA2>
 A:Cross-references: EMBL:S68026
 A:Note: the authors translated the codon GAC for residue 170 as Glu
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
 C:Keywords: ATP; transmembrane protein
 F:675-941/Domain: protein kinase homology <KIN>
 F:683-691/Region: protein kinase ATP-binding motif

Query Match 43.2%; Score 57; DB 2; Length 1005;
 Best Local Similarity 57.9%; Pred. No. 5;
 Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 |||||: ||: |||||
 Db 596 LSGSCCEGCGRA--SSLC 612

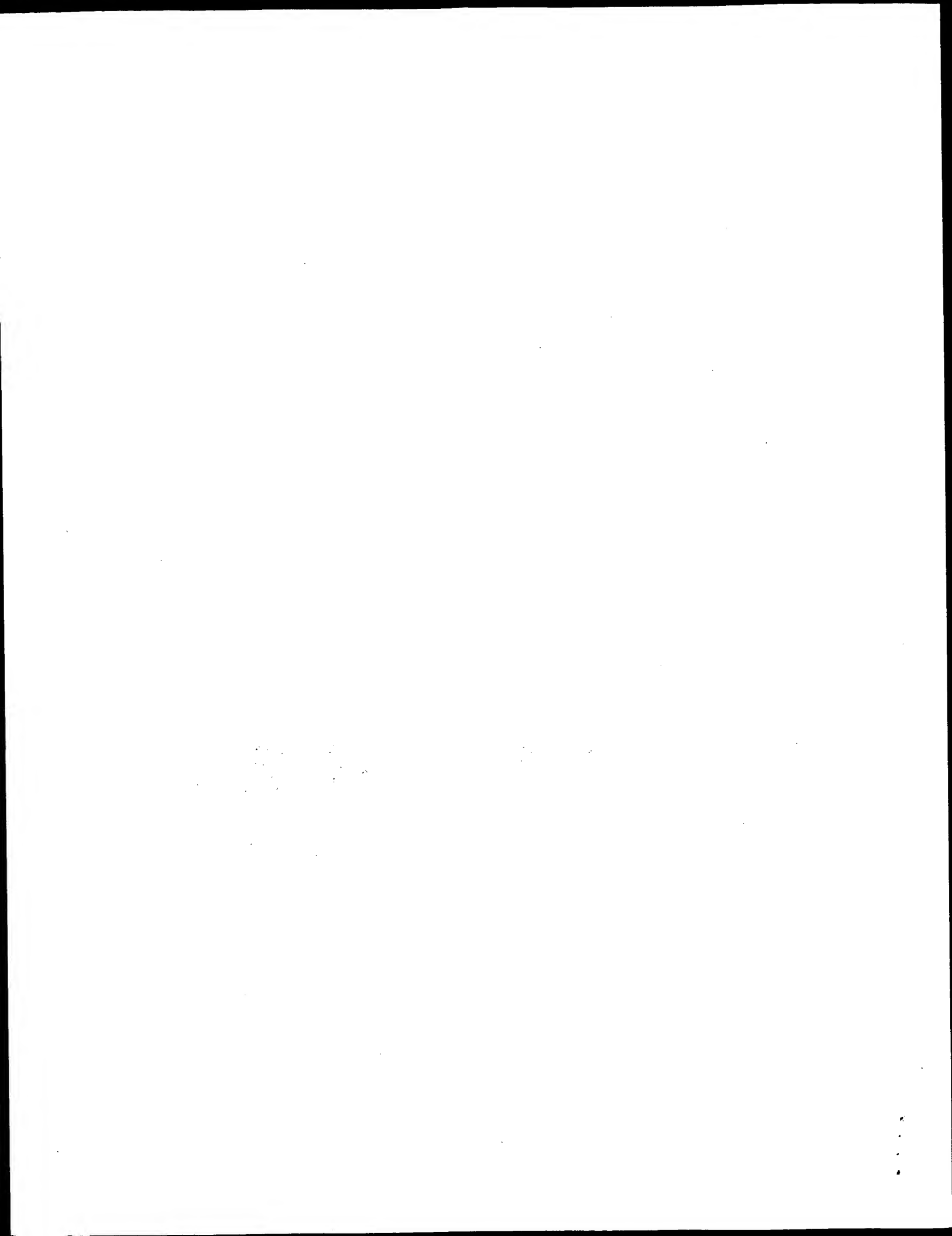
RESULT 13
 S42776
 relaxin - baboon (fragment)
 C:Species: Papio sp. (baboon)
 C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: S42776
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42776
 A:Molecule type: DNA
 A:Residues: 1-24 <EVA>
 A:Cross-references: EMBL:Z27106; NID:g415396; PIDN:CAA81622.1; PID:g415397
 C:Genetics:
 C:Superfamily: insulin
 C:Keywords: disulfide bond; hormone
 F:1-24/Domain: relaxin chain A (fragment) #status predicted <RXA>

Query Match 42.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 42.1%; Pred. No. 0.36;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
 ||: || ||: ||: ||
 Db 6 LSNKCHIGCTKKLAKFC 24

RESULT 14
 T37327
 insulin homolog ceinsulin-3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-Jan-2000
 C:Accession: T37327; T15535
 R:Kawano, T.
 submitted to the EMBL Data Library, September 1999
 A:Description: MRNA for a putative insulin-like peptide of Caenorhabditis elegans.
 A:Reference number: Z21691
 A:Accession: T37327
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-91 <KAW>
 A:Cross-references: EMBL:AB032258; PIDN:BA84470.1
 R:Du, Z.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C17C3.
 A:Reference number: Z18366
 A:Accession: T15535
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA

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Job time: 212 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:16:52 ; Search time 18.68 seconds
(without alignments)
49.747 Million cell updates/sec

Title: US-09-781-077-2_COPY_119_142
Perfect score: 132
Sequence: 1 DVLGLSSCKWGCKSKSEISL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 74 | 56.1 | 54 | 1 RELX_SQUAC | P11953 squalus aca |
| 2 | 66 | 50.0 | 182 | 1 RELX_HORSE | P22969 equus caball |
| 3 | 63 | 47.7 | 44 | 1 RELX_ODOTA | P01349 odontaspis |
| 4 | 63 | 47.7 | 135 | 1 INLS_MOUSE | Q9wug6 mus musculus |
| 5 | 61 | 46.2 | 213 | 1 INL6_HUMAN | Q9y581 homo sapien |
| 6 | 59.5 | 45.1 | 129 | 1 C59B_MOUSE | P58019 mus musculus |
| 7 | 59 | 44.7 | 188 | 1 INL6_RAT | Q9wv41 rattus norv |
| 8 | 58 | 43.9 | 54 | 1 RELX_BALAC | P11184 balaenopter |
| 9 | 58 | 43.9 | 54 | 1 RELX_BALED | P11185 balaenopter |
| 10 | 58 | 43.9 | 182 | 1 RELX_PIG | P01348 sus scrofa |
| 11 | 57 | 43.2 | 135 | 1 INLS_HUMAN | Q9y5q6 homo sapien |
| 12 | 57 | 43.2 | 177 | 1 RELX_CANFA | Q9trm8 canis famil |
| 13 | 57 | 43.2 | 186 | 1 RELX_RAT | P01347 rattus norv |
| 14 | 57 | 43.2 | 1005 | 1 EPA5_RAT | P54757 rattus norv |
| 15 | 57 | 43.2 | 1037 | 1 EPA5_HUMAN | P54756 homo sapien |
| 16 | 56 | 42.4 | 91 | 1 ILGL_CABEL | Q18060 caenorhabdi |
| 17 | 56 | 42.4 | 185 | 1 RELX_MACMU | P19884 macaca mula |
| 18 | 55 | 41.7 | 877 | 1 EPA5_MOUSE | Q60629 mus musculus |
| 19 | 54 | 40.9 | 191 | 1 INL6_MOUSE | Q9qv05 mus musculus |
| 20 | 53.5 | 40.5 | 75 | 1 MIH_PROCL | P55848 procamburus |
| 21 | 53 | 40.2 | 221 | 1 YMI7_PARTE | P15618 paramacium |
| 22 | 52 | 39.4 | 145 | 1 LMR1_LOEMI | P15131 locusta mig |
| 23 | 52 | 39.4 | 166 | 1 REL2_PANTR | P51455 pan troglod |
| 24 | 52 | 39.4 | 185 | 1 REL2_HUMAN | P04090 homo sapien |
| 25 | 51 | 38.6 | 63 | 1 V7K_BYDVP | P09517 barley yell |
| 26 | 51 | 38.6 | 81 | 1 RELX_DASSA | P81191 dasyatis sa |
| 27 | 49 | 37.1 | 64 | 1 RELX_RAJER | P11952 raja erinac |
| 28 | 49 | 37.1 | 131 | 1 INL3_CALJA | Q97937 callithrix |
| 29 | 49 | 37.1 | 169 | 1 KRUH_HUMAN | P26371 homo sapien |
| 30 | 49 | 37.1 | 185 | 1 RELX_MESAU | Q64171 mesocricetu |
| 31 | 49 | 37.1 | 185 | 1 RELX_MOUSE | P47932 mus musculus |
| 32 | 49 | 37.1 | 2871 | 1 FBNI_MOUSE | Q61554 mus musculus |
| 33 | 49 | 37.1 | 2871 | 1 FBNI_PIG | Q9lv36 sus scrofa |

34 48 36.4 60 1 MT_ESOLU
35 48 36.4 134 1 INLI_DROME
36 48 36.4 160 1 RELX_CAVPO
37 47 35.6 50 1 INS2_BATSP
38 47 35.6 51 1 INS_ORNAN
39 47 35.6 60 1 MT2_CYPCA
40 47 35.6 60 1 MTA_CYP51
41 47 35.6 60 1 MTA_SPAU
42 47 35.6 60 1 MT_BRARE
43 47 35.6 60 1 MT_CARAU
44 47 35.6 60 1 MT_ICTPU
45 47 35.6 60 1 MT_NOEBA

ALIGNMENTS

RESULT 1
RELX_SQUAC
AC P11953; STANDARD; PRT; 54 AA.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE
RC TISSUE-Ovary;
RX MEDLINE=87054035; PubMed=3780747;
RA Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
RA Callard I.P.;
RT "Isolation, purification, and the sequence of relaxin from spiny
dogfish (Squalus acanthias).";
RL Eur. J. Biochem. 161:335-341(1986).
CC -!- FUNCTION: THE FUNCTION OF RELAXIN IN AN OVIPAROUS SPECIES IS NOT
YET KNOWN.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR; A26463; A26463.
DR PIR; B26463; B26463.
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 30 RELAXIN B CHAIN.
FT NON_CONS 30 31
FT CHAIN 31 54 RELAXIN A CHAIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFD 13 41 INTERCHAIN.
FT DISULFD 25 54 INTERCHAIN.
FT DISULFD 40 45
SQ SEQUENCE 54 AA; 5910 MW; 1B7206773AD32A5B CRC64;

Query Match 56.1%; Score 74; DB 1; Length 54;
Best Local Similarity 55.0%; Pred. No. 0.00028;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GLSSCKCKWGCKSKSEISL 24
I::I I::I::I::I::I
Db 35 GMSKCKCTYGTCKDKISL 54

RESULT 2
RELX_HORSE


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QY 5 GLSSCKWGCSEISL 24
   |||||
Db 173 GYSEKCLTGCTKEELSIAC 192

RESULT 6
C59B_MOUSE
ID C59B_MOUSE STANDARD; PRT; 129 AA.
AC P58019;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD59B glycoprotein precursor (Membrane attack complex inhibition
factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20403635; PubMed=10946279;
RA Qian Y.-M., Qin X., Miwa T., Sun X., Halperin J.A., Song W.-C.;
RT *Identification and functional characterization of a new gene encoding
the mouse terminal complement inhibitor CD59.*;
RL J. Immunol. 165:2528-2534(2000).
CC -!- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
COMPLEMENTS OF THE ASSEMBLING MAC, THEREBY PREVENTING
INCORPORATION OF THE MULTIPLE COPIES OF C9 REQUIRED FOR COMPLETE
FORMATION OF THE OSMOLYTIC PORE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: SPECIFICALLY IN TESTIS.
CC -!- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
DR MGD; MG1:188996; CD59B.
DR InterPro: IPR001526; LY6_UPAR.
DR Pfam: PF00021; UPAR_LY6; 1.
DR ProDom: PD003128; LY6_CD59; 1.
DR SMART; SM00134; L0; 1.
DR PROSITE; PS00983; LY6_UPAR; FALSE_NEG.
KW Antigen; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 107 CD59B GLYCOPROTEIN.
FT PROPEP 108 129 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 24 107 UPAR/LY6.
FT DISULFID 26 49 BY SIMILARITY.
FT DISULFID 29 36 BY SIMILARITY.
FT DISULFID 42 62 BY SIMILARITY.
FT DISULFID 68 86 BY SIMILARITY.
FT DISULFID 87 92 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
FT LIPID 107 107 GPI-ANCHOR (BY SIMILARITY).
SQ SEQUENCE 129 AA; 14266 MW; 2D619096AA9C9CEE CRC64;

Query Match 45.1%; Score 59.5; DB 1; Length 129;
Best Local Similarity 40.6%; Pred. No. 0.071;
Matches 13; Conservative 5; Mismatches 3; Indels 11; Gaps 2;

QY 3 LAGLSCKWGCSEISL 23
   |||||
Db 79 VAGIQSKCCWGLCNKLDGLPEPNAETSSL 110

RESULT 7
INL6_RAT
ID INL6_RAT STANDARD; PRT; 188 AA.
AC Q9W41;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Insulin-like peptide INSL6 precursor (Insulin-like peptide 6).
INSL6.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20297000; PubMed=10819760;
RA Lok S., Johnston D.S., Conklin D., Lofton-Day C.E., Adams R.L.,
Jelmsberg A.C., Whitmore T.E., Schrader S., Griswold M.D.,
Jaspers S.R.;
RT *Identification of INSL6, a new member of the insulin family that is
expressed in the testis of the human and Rat.*;
RL Biol. Reprod. 62:1593-1599(2000).
CC -!- FUNCTION: MAY HAVE A ROLE IN SPERM DEVELOPMENT AND FERTILIZATION.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: TESTIS- AND PROSTATE-SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC
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CC
EMBL: AF159506; AAD40956.1;
InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 188 INSULIN-LIKE PEPTIDE INSL6.
FT CHAIN 23 51 INSULIN-LIKE PROTEIN INSL6 B CHAIN
(POTENTIAL).
FT PROPEP 53 158 INSULIN-LIKE PROTEIN INSL6 C CHAIN
(POTENTIAL).
FT CHAIN 163 188 INSULIN-LIKE PROTEIN INSL6 A CHAIN
(POTENTIAL).
FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT DISULFID 33 169 BY SIMILARITY.
FT DISULFID 45 182 BY SIMILARITY.
FT DISULFID 168 173 BY SIMILARITY.
SQ SEQUENCE 188 AA; 21442 MW; 50212AB3CE9982B3 CRC64;

Query Match 44.7%; Score 59; DB 1; Length 188;
Best Local Similarity 45.0%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 GLSSCKWGCSEISL 24
   |||||
Db 163 GFADKCAIGCSREELAVAC 182

RESULT 8
RELX_BALAC
ID RELX_BALAC STANDARD; PRT; 54 AA.
AC P1184;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;

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RN SEQUENCE.
RX MEDLINE=89093167; PubMed=2910872;
RA Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.;
RT "Cetacean relaxin. Isolation and sequence of relaxins from
RT Balaenoptera acutorostrata and Balaenoptera edeni.";
RL J. Biol. Chem. 264:940-943(1989).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR: B32201; B32201.
DR HSP: P01348; 4RLX.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; ILGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 32 RELAXIN B CHAIN.
FT NON_CONS 32 33
FT CHAIN 33 54 RELAXIN A CHAIN.
FT DISULFID 10 41 INTERCHAIN.
FT DISULFID 22 54 INTERCHAIN.
FT DISULFID 40 45
SQ SEQUENCE 54 AA; 6099 MW; DC2672CB940F59BE CRC64;

Query Match 43.9%; Score 58; DB 1; Length 54;
Best Local Similarity 47.4%; Pred. NO. 0.055;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISSLC 24
|| || : || : || : ||
Db 36 LSEKCCQVGCIRKDIARLC 54

RESULT 9
RELX_BALED STANDARD; PRT; 54 AA.
AC P11185;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Relaxin.
OS Balaenoptera edeni (Bryde's whale).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9769;
RN [1]
RP SEQUENCE.
RX MEDLINE=89093167; PubMed=2910872;
RA Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.;
RT "Cetacean relaxin. Isolation and sequence of relaxins from
RT Balaenoptera acutorostrata and Balaenoptera edeni.";
RL J. Biol. Chem. 264:940-943(1989).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR PIR: A32201; A32201.
DR HSP: P01348; 4RLX.
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; ILGF; 1.
DR PROSITE: PS00262; INSULIN; 1.
KW Insulin family; Hormone.
FT CHAIN 1 32 RELAXIN B CHAIN.
FT NON_CONS 32 33

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FT CHAIN 33 54 RELAXIN A CHAIN.
FT DISULFID 10 41 INTERCHAIN.
FT DISULFID 22 54 INTERCHAIN.
FT DISULFID 40 45
SQ SEQUENCE 54 AA; 6072 MW; DB5535F8951F49BE CRC64;

Query Match 43.9%; Score 58; DB 1; Length 54;
Best Local Similarity 47.4%; Pred. NO. 0.055;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCKSKSEISSLC 24
|| || : || : || : ||
Db 36 LSEKCCQVGCIRKDIARLC 54

RESULT 10
RELX_PIG STANDARD; PRT; 182 AA.
AC P01348;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Porrelaxin precursor.
GN RLN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87308187; PubMed=2442155;
RA Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
RA Niall H.;
RT "Porcine relaxin. Gene structure and expression.";
RL J. Biol. Chem. 262:11940-11946(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157118; PubMed=6897721;
RA Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
RA Tregear G., Niall H.;
RT "Porcine relaxin: molecular cloning and cDNA structure.";
RL DNA 1:155-162(1982).
RN [3]
RP PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
RX MEDLINE=77213067; PubMed=876374;
RA James R., Niall H., Kwok S., Bryant-Greenwood G.;
RT "Primary structure of porcine relaxin: homology with insulin and
RT related growth factors.";
RL Nature 267:544-546(1977).
RN [4]
RP SEQUENCE OF 25-51.
RX MEDLINE=77157271; PubMed=851452;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the B-chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 75:503-510(1977).
RN [5]
RP SEQUENCE OF 25.
RX MEDLINE=77134136; PubMed=843375;
RA Schwabe C., McDonald J.K.;
RT "Demonstration of a pyroglutamyl residue at the N terminus of the B-
RT chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 74:1501-1504(1977).
RN [6]
RP SEQUENCE OF 161-182.
RX MEDLINE=76231539; PubMed=938497;
RA Schwabe C., McDonald J.K., Steinetz B.G.;
RT "Primary structure of the A chain of porcine relaxin.";
RL Biochem. Biophys. Res. Commun. 70:397-405(1976).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77236040; PubMed=887933;
RA Schwabe C., McDonald J.K.;

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RT "Relaxin: a disulfide homolog of insulin.";
RL Science 197:914-915(1977).
RN [8]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=78092399; PubMed=622170;
RA Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G.,
RA Evans A., North A.C.T.;
RT "Relaxin and its structural relationship to insulin.";
RL Nature 271:278-281(1978).
CC -1- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
CC TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC -----
DR EMBL; K01088; AAA31114.1; -
DR EMBL; J02792; AAA31115.1; -
DR EMBL; A16593; CAA01295.1; -
DR EMBL; A06852; CAA00600.1; -
DR PIR; A01615; RXPG.
DR PIR; A29796; A29796.
DR PDB; 1RLX; 15-OCT-94.
DR PDB; 2RLX; 15-OCT-94.
DR PDB; 3RLX; 15-OCT-94.
DR PDB; 4RLX; 15-OCT-94.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 56
FT PROPEP 57 154
FT CHAIN 161 182
FT MOD_RES 25 25
FT DISULFID 34 169
FT DISULFID 46 182
FT DISULFID 168 173
FT CONFLICT 47 47
FT CONFLICT 51 54
FT CONFLICT 116 116
FT CONFLICT 170 170
FT CONFLICT 176 176
FT SEQUENCE 182 AA; 20818 MW; 20736EB089F13AB4 CRC64;
SQ

Query Match 43.98; Score 58; DB 1; Length 182;
Best Local Similarity 47.4%; Pred. No. 0.16;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
DB 164 LSEKCCQVGCIRKDIARLC 182
II ||: ||: ||: ||: ||: ||

RESULT 11
INL5_HUMAN
ID INL5_HUMAN STANDARD; PRT; 135 AA.
AC 09Y506.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
GN INSL5.
OS Homo sapiens (Human).

"Relaxin: a disulfide homolog of insulin.";
Science 197:914-915(1977).
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE-Colon;
RX MEDLINE=99389725; PubMed=10458910;
RA Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
RA Lok S., Jaspers S.;
RT "Identification of INSL5, a new member of the insulin superfamily.";
RL Genomics 60:50-56(1999).
CC -1- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
CC DEVELOPMENT AND REGULATION.
CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS
CC IN UTERUS AND ASCENDING AND DESCENDING COLON.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF133816; AAD29686.1; -
DR MIM; 606413; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 18
FT CHAIN 19 48
FT PROPEP 49 114
FT CHAIN 115 135
FT DISULFID 29 122
FT DISULFID 41 135
FT DISULFID 121 126
FT SEQUENCE 135 AA; 15318 MW; 98FFCB20E9C4BC1F CRC64;
SQ

Query Match 43.2%; Score 57; DB 1; Length 135;
Best Local Similarity 47.4%; Pred. No. 0.17;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 LSSSCCKWGCCKSKSEISSLC 24
DB 117 LQFLCCTDGCSTMDLSALC 135
II: || ||: ||: ||: ||: ||: ||

RESULT 12
RELX_CANFA
ID RELX_CANFA STANDARD; PRT; 177 AA.
AC 09TRM8; 09TRM9; Q9N0Z7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Prorelaxin precursor.
GN RLN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=99150177; PubMed=10026098;
RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
RA Steger K., Steinetz B.G., Fischer B.;

```

1000

[2] SEQUENCE FROM N.A. (ISOFORM 6).
STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
MEDLINE=95206467; PubMed=7898646;
Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
Lassmann H., Steck A.J.;
"Expression and developmental regulation of Etk-1, a neuronal
Etk-like receptor tyrosine kinase in brain."
Neuroscience 63:163-178(1994).
-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND
6; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
SYSTEM. PROMINANTLY EXPRESSED IN NEURONS.
-1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.

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EMBL; X78689; CAA55357.1; -
HSP; P29323; 18AF
InterPro; IPR000561; EGF-like.
InterPro; IPR001090; Ephrin-receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR001426; Receptor_tyr_kin_v.
InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF01404; EPH_1bd; 1.
Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
ProDom; PD001495; Ephrin_rceptor; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00060; FN3; 2.
SMART; SM00219; TyRK; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS0105; SAM_DOMAIN; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Alternative splicing.
SIGNAL 1 26
CHAIN 27 1005
DOMAIN 27 575
FT DOMAIN 576 596
FT TRANSMEM 597 1005
FT DOMAIN 222 356
FT DOMAIN 357 466
FT DOMAIN 467 563
FT DOMAIN 677 938
FT DOMAIN 967 1005
FT NP_BIND 683 691
FT BINDING 709 709
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).

FT ACT_SITE 802
FT MOD_RES 652
FT MOD_RES 658
FT MOD_RES 835
FT MOD_RES 835
FT MOD_RES 984
FT CARBOHYD 266
FT CARBOHYD 301
FT CARBOHYD 371
FT CARBOHYD 425
FT CARBOHYD 438
FT CARBOHYD 463
FT VARSPLIC 10
FT VARSPLIC 306
FT VARSPLIC 357
FT VARSPLIC 358
FT VARSPLIC 470
FT VARSPLIC 597
FT CONFLICT 170
FT CONFLICT 566
FT CONFLICT 578
FT CONFLICT 669
FT CONFLICT 708
FT CONFLICT 979
FT SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
Query Match 43.2%; Score 57; DB 1; Length 1005;
Best Local Similarity 57.9%; Pred. No. 0.94;
Matches 11; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 6 LSSCCCKWCKSKSEISSLC 24
Db 596 LSGSCCECGCGRA--SSLC 612
RESULT 15
EPAS_HUMAN
ID EPAS_HUMAN STANDARD; PRT; 1037 AA.
AC P54756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein-
DE kinase receptor EHK-1) (Eph homology kinase-1) (Receptor protein-
DE tyrosine kinase HEK7).
GN EPAS OR EHK1 OR HEK7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Miescher G.C.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN
RP SEQUENCE OF 25-1037 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95206782; PubMed=7898931;
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA Basu R., Welcher A.A.;
RT "cDNA cloning and tissue distribution of five human EPH-like receptor
RT protein-tyrosine kinases."
RL Oncogene 10:897-905(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:16:29 ; Search time 58.57 Seconds
(without alignments)
70.887 Million cell updates/sec

Title: US-09-781-077-2_COPY_119_142

Perfect score: 132

Sequence: 1 DVLAGSSCCCKWCKSKSEISL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 63 | 47.7 | 155 | 13 | Q9DEP8 |
| 2 | 58 | 43.9 | 22 | 6 | Q9TRG6 |
| 3 | 57 | 43.2 | 180 | 6 | Q9MYK8 |
| 4 | 56 | 42.4 | 24 | 6 | Q28787 |
| 5 | 56 | 42.4 | 199 | 6 | Q9NOT9 |
| 6 | 52.5 | 39.8 | 129 | 11 | Q920G7 |
| 7 | 52 | 39.4 | 24 | 6 | Q28430 |
| 8 | 52 | 39.4 | 24 | 6 | Q28781 |
| 9 | 51.5 | 39.0 | 868 | 5 | Q9WIA5 |
| 10 | 51 | 38.6 | 262 | 10 | Q9LV78 |
| 11 | 51 | 38.6 | 370 | 5 | Q95VP6 |
| 12 | 51 | 38.6 | 1159 | 16 | Q9HYX0 |
| 13 | 50 | 37.9 | 399 | 5 | O62189 |
| 14 | 50 | 37.9 | 823 | 5 | Q23141 |
| 15 | 49.5 | 37.5 | 448 | 10 | Q9LZV3 |
| 16 | 49 | 37.1 | 169 | 4 | Q14564 |

| | | | | | |
|----|------|------|------|----|--------|
| 17 | 49 | 37.1 | 272 | 11 | Q99L19 |
| 18 | 49 | 37.1 | 362 | 11 | O35281 |
| 19 | 49 | 37.1 | 2872 | 11 | Q9WUH8 |
| 20 | 49 | 37.1 | 3857 | 11 | O88840 |
| 21 | 48 | 36.4 | 56 | 5 | Q9SSZ7 |
| 22 | 48 | 36.4 | 127 | 13 | Q90WX8 |
| 23 | 48 | 36.4 | 188 | 6 | Q9GK46 |
| 24 | 48 | 36.4 | 332 | 10 | O65485 |
| 25 | 48 | 36.4 | 444 | 12 | Q9VTK1 |
| 26 | 48 | 36.4 | 459 | 4 | Q92577 |
| 27 | 48 | 36.4 | 686 | 4 | Q15061 |
| 28 | 48 | 36.4 | 2233 | 5 | Q94711 |
| 29 | 47.5 | 36.0 | 205 | 5 | Q9BK18 |
| 30 | 47.5 | 36.0 | 735 | 11 | Q9D4G3 |
| 31 | 47.5 | 36.0 | 735 | 11 | Q9OWJ0 |
| 32 | 47.5 | 36.0 | 735 | 11 | O60718 |
| 33 | 47.5 | 36.0 | 2809 | 4 | Q96JP8 |
| 34 | 47 | 35.6 | 108 | 5 | Q20896 |
| 35 | 47 | 35.6 | 118 | 10 | Q9S979 |
| 36 | 47 | 35.6 | 131 | 6 | Q9N0Z8 |
| 37 | 47 | 35.6 | 131 | 6 | Q9N0T8 |
| 38 | 47 | 35.6 | 131 | 6 | Q9GK47 |
| 39 | 47 | 35.6 | 179 | 5 | O23203 |
| 40 | 47 | 35.6 | 195 | 5 | O16759 |
| 41 | 47 | 35.6 | 251 | 5 | Q9T225 |
| 42 | 47 | 35.6 | 464 | 10 | Q41064 |
| 43 | 47 | 35.6 | 718 | 3 | Q96VZ6 |
| 44 | 47 | 35.6 | 2621 | 10 | Q9LM23 |
| 45 | 47 | 35.6 | 2658 | 10 | Q9SGE4 |

ALIGNMENTS

RESULT 1

Q9DEP8 ID Q9DEP8 PRELIMINARY; PRT; 155 AA.
AC Q9DEP8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
GN INSL3.
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21309007; PubMed=11416046;
RA De Rienzo G., Aniello F., Branno M., Minucci S.;
RT "Isolation and characterization of a novel member of the relaxin/insulin family from the testis of the frog Rana esculenta.";
RL Endocrinology 142:3231-3238(2001).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL: AJ298874; CAC16108.1;
DR InterPro: IPR000739; Insulin_IGF_relaxin.
DR InterPro: IPR002052; N6_Mtase.
DR Pfam: PF00049; Insulin; 1.
DR SMART: SM00078; ILGF; 1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 155 AA; 17470 MW; 517ADA5385026E34 CRC64;

Query Match Best Local Similarity 47.7%; Score 63; DB 13; Length 155;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 AGLSSCCCKWCKSKSEISL 24
DB 135 AGPALSCCQRCQCTKRLMKFC 155

Best Local Similarity 44.4%; Pred. NO. 0.21;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 SSSCCCKWGCSEISSLC 24
DB 163 SDRCCNVGCTRELADLC 180

RESULT 4
ID Q28787 PRELIMINARY; PRT; 24 AA.
AC Q28787;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN (FRAGMENT).
GN RLX.

OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.

OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BABA;
RA Evans B.B.A., Fu P., Tregear G.G.W.;
RT "Characterisation of primate relaxin genes."
RL J. Mol. Endocrinol. 0:0-0(1993).

CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

DR EMBL; Z27106; CAA81622.1; -.

DR HSP; P04090; 6RLX.

DR InterPro; IPR000739; Insulin_IGF_relaxin.

DR PROSITE; PS00262; INSULIN; 1.

FT NON_TER 1

SQ SEQUENCE 24 AA; 2691 MW; 560BC26A8BADBA14 CRC64;

Query Match 42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. NO. 0.042;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 LSSCCCKWGCSEISSLC 24
DB 6 LSNKCHIGCTKSLAKFC 24

RESULT 5
ID Q9N0T9 PRELIMINARY; PRT; 199 AA.
AC Q9N0T9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PREPRORELAXIN.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20191540; PubMed=10727251;
RA Hombach-Klonisch S., Abd-Elnaeim M., Skidmore J.A., Leiser R.,
RA Fischer B., Klonisch T.;
RT "Ruminant relaxin in the pregnant one-humped camel."
RL Biol. Reprod. 62:839-846(2000).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

DR EMBL; AF254739; AAF67741.1; -.

DR HSP; P01348; 1RLX.

DR InterPro; IPR000739; Insulin_IGF_relaxin.

DR SMART; SM00078; IIGF; 1.

DR PROSITE; PS00262; INSULIN; 1.

RESULT 2
ID Q9TRG6 PRELIMINARY; PRT; 22 AA.
AC Q9TRG6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN R-III A CHAIN.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.

RA MEDLINE=93257096; PubMed=8489740;

RA Kohsaka T., Takahara H., Sugawara K., Tagami S.;

RT "Endogenous heterogeneity of relaxin and sequence of the major form in

pregnant sow ovaries."

RL Biol. Chem. Hoppe-Seyler 374:203-210(1993).

CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

DR HSP; P01348; 1RLX.

DR InterPro; IPR000739; Insulin_IGF_relaxin.

DR PROSITE; PS00262; INSULIN; 1.

SQ SEQUENCE 22 AA; 2527 MW; F4DB254222449313 CRC64;

Query Match 43.9%; Score 58; DB 6; Length 22;
Best Local Similarity 47.4%; Pred. NO. 0.018;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 LSSCCCKWGCSEISSLC 24
DB 4 LSEKCCQVCIRKIDARLC 22

RESULT 3
ID Q9MYK8 PRELIMINARY; PRT; 180 AA.
AC Q9MYK8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RELAXIN
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99115216; PubMed=9915995;
RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
RA Steger K., Huppertz B., Fischer B.;
RT "Nucleic acid sequence of feline preprorelaxin and its localization within the feline placenta."
RL Biol. Reprod. 60:305-311(1999).

CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

DR EMBL; AF233688; AAF60303.1; -.

DR HSP; P04090; 6RLX.

DR InterPro; IPR000739; Insulin_IGF_relaxin.

DR SMART; SM00078; IIGF; 1.

DR PROSITE; PS00262; INSULIN; 1.

SQ SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;

Query Match 43.2%; Score 57; DB 6; Length 180;

100

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).

CC -I- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
 CC -I- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

DR EMBL; AE004749; AAG06659.1; -;
 DR InterPro: IPR004358; BCTRLSENSOR.
 DR InterPro: IPR003594; HATPase_c.
 DR InterPro: IPR003661; HIS_kinA.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR001734; Na_solut_sympo.
 DR InterPro: IPR000014; PAS.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PRO0344; BCTRLSENSOR.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HSKA; 1.
 DR SMART; SM00091; PAS; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW Transference.
 SQ SEQUENCE 1159 AA; 127452 MW; 1C4D145CE0E190CF CRC64;

Query Match 38.6%; Score 51; DB 16; Length 1159;
 Best Local Similarity 35.7%; Pred. No. 12;
 Matches 10; Conservative 7; Mismatches 5; Indels 6; Gaps 1;

QY 2 VLAGLSSCCCKWGC-----SKSETSSL 23
 DB 1050 ILAGMNSLLSRGQCVWTARSRECATL 1077

RESULT 13
 ID O62189 PRELIMINARY; PRT; 399 AA.
 AC O62189;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F31B9.1 PROTEIN.
 GN F31B9.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Steward C.A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RL EMBL; Z81520; CAB04223.1; -;
 DR InterPro: IPR002106; AA_CRNA_ligase_II.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
 SQ SEQUENCE 399 AA; 45577 MW; 83FF18CF47A7CF88 CRC64;

Query Match 37.9%; Score 50; DB 5; Length 399;
 Best Local Similarity 59.1%; Pred. No. 6.1;

Matches 13; Conservative 1; Mismatches 4; Indels 4; Gaps 2;
 QY 1 DVLAGLSSCCCKW--GCSKSE 19
 DB 343 DVAAGISSFCC-WLLPFSKSE 363

RESULT 14
 ID Q23141 PRELIMINARY; PRT; 823 AA.
 AC Q23141;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 95.3 KDA PROTEIN.
 GN W03B1.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Miller N., Bradshaw H., Wu X., Gattung S.;
 RT "The sequence of C. elegans cosmid W03B1.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58753; AAC24437.1; -;
 DR InterPro: IPR002111; Cat_channel_TrpL.
 KW Hypothetical protein.
 SQ SEQUENCE 823 AA; 95286 MW; 5AC484962DCDD7D4 CRC64;

Query Match 37.9%; Score 50; DB 5; Length 823;
 Best Local Similarity 61.1%; Pred. No. 12;
 Matches 11; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 6 LSSSCCKGCKSKSEISSL 23
 DB 664 LTSGCCK--CSSTAISL 679

RESULT 15
 ID Q9LZV3 PRELIMINARY; PRT; 448 AA.
 AC Q9LZV3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE (1-4)-BETA-MANNAN ENDOHYDROLASE-LIKE PROTEIN.
 GN T20115.200.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Van Den Daele H.,

RA Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lencke K., Mayer K.F.X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases..
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162351; CAB82763.1; -;
 DR InterPro: IPR000886; ER_target.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 448 AA; 50622 MW; 977B341312A54D7D CRC64;

Query Match 37.5%; Score 49.5; DB 10; Length 448;
 Best Local Similarity 41.7%; Pred. No. 8.2;
 Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

QY 3 LAGLSSSC---CKWGCSKSEISL 23
 || :| | | | | :|
 Db 416 LAIFNSLCSWRCRWGCKKKNQTAL 439

Search completed: June 27, 2002, 16:16:31
 Job time: 500 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:08 ; Search time 73.16 Seconds
(without alignments)
40.992 Million cell updates/sec

Title: US-09-781-077-2_COPY_26_52

Perfect score: 150

Sequence: 1 RAAFYGVRLCGREFIRAVIFTCGSRW 27

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
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12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 150 | 100.0 | 142 | 22 | AA198114 |
| 2 | 87 | 58.0 | 40 | 17 | AA196006 |
| 3 | 82 | 54.7 | 30 | 20 | AA191963 |
| 4 | 82 | 54.7 | 31 | 21 | AA195773 |
| 5 | 82 | 54.7 | 135 | 19 | AA197925 |
| 6 | 82 | 54.7 | 135 | 20 | AA191961 |
| 7 | 82 | 54.7 | 135 | 21 | AA190173 |
| 8 | 82 | 54.7 | 135 | 21 | AA1924391 |
| 9 | 82 | 54.7 | 135 | 21 | AA195770 |
| 10 | 82 | 54.7 | 135 | 21 | AA1983228 |
| 11 | 82 | 54.7 | 135 | 22 | AA1924033 |

| | | | | | | |
|----|----|------|-----|----|-----------|---------------------|
| 12 | 82 | 54.7 | 135 | 22 | AA192309 | Human PRO182 polyp |
| 13 | 82 | 54.7 | 135 | 22 | AA1920110 | Human immunostimul |
| 14 | 82 | 54.7 | 135 | 22 | AA193072 | Human angioestesis |
| 15 | 76 | 50.7 | 31 | 18 | AA197863 | Relaxin-like facto |
| 16 | 75 | 50.0 | 135 | 19 | AA197926 | Mouse Zins3 protei |
| 17 | 75 | 50.0 | 135 | 21 | AA195771 | Mouse insulin fami |
| 18 | 74 | 49.3 | 46 | 21 | AA196172 | Human Rlf partial |
| 19 | 71 | 47.3 | 29 | 16 | AA194894 | Human relaxin B-ch |
| 20 | 71 | 47.3 | 29 | 16 | AA197942 | Human relaxin B-ch |
| 21 | 71 | 47.3 | 46 | 11 | AA195208 | Ubiquitin C-termin |
| 22 | 71 | 47.3 | 114 | 11 | AA195207 | Ubiquitin-relaxin |
| 23 | 71 | 47.3 | 162 | 11 | AA197987 | H2 prorelaxin gene |
| 24 | 71 | 47.3 | 162 | 11 | AA197988 | H2 prorelaxin dedu |
| 25 | 71 | 47.3 | 185 | 5 | AA1940108 | Sequence of human |
| 26 | 71 | 47.3 | 185 | 5 | AA1940154 | Sequence of human |
| 27 | 71 | 47.3 | 185 | 5 | AA1940155 | Amino acid sequenc |
| 28 | 71 | 47.3 | 185 | 10 | AA194621 | Amino acid sequenc |
| 29 | 71 | 47.3 | 185 | 10 | AA194622 | Angiotensin conver |
| 30 | 71 | 47.3 | 220 | 22 | AA192911 | Asymmetry sequenc |
| 31 | 69 | 46.0 | 33 | 17 | AA196004 | Relaxin analogue B |
| 32 | 68 | 45.3 | 29 | 18 | AA19305 | Human relaxin part |
| 33 | 66 | 44.0 | 46 | 21 | AA196171 | Relaxin B-chain. |
| 34 | 64 | 42.7 | 52 | 16 | AA194905 | Sequence of porcine |
| 35 | 55 | 36.7 | 182 | 4 | AA1930392 | Sequence of porcine |
| 36 | 55 | 36.7 | 182 | 5 | AA1940156 | Human secreted pro |
| 37 | 53 | 35.3 | 86 | 21 | AA197065 | Human gene 2 encod |
| 38 | 53 | 35.3 | 86 | 22 | AA196042 | Caenorhabditis ele |
| 39 | 53 | 35.3 | 106 | 21 | AA196140 | C. elegans insulin |
| 40 | 53 | 35.3 | 106 | 21 | AA195656 | Human secreted pro |
| 41 | 53 | 35.3 | 108 | 21 | AA197157 | Human gene 2 encod |
| 42 | 53 | 35.3 | 108 | 22 | AA196134 | Prorelaxin fragme |
| 43 | 53 | 35.3 | 150 | 16 | AA1964904 | Human polypeptide |
| 44 | 53 | 35.3 | 187 | 22 | AA193246 | Rat Zins2 testis-s |
| 45 | 53 | 35.3 | 188 | 19 | AA1947547 | |

ALIGNMENTS

RESULT 1
AAG78114
ID AAG78114 standard; Protein; 142 AA.
XX AC AAG78114;
XX DT 21-NOV-2001 (first entry)
XX DE Human insulin homologue polypeptide Zins4.
XX KW Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic;
KW antifertility; vasotropic; reproductive disorder; prostate disorder;
KW heart disorder; kidney disorder; gonadal development; pregnancy;
KW pubertal change; menopause; ovarian cancer; testicular cancer; ovulation;
KW polycystic ovarian syndrome; contractile tissue; cardiovascular disease;
KW birth control; impotence; myocyte; endothelial cell; osteoblast;
KW blood pressure; muscle tension; osmotic balance; gene therapy.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
FT Peptide 1..25
FT Protein /label= signal_peptide
FT 26..142 /label= mature_protein
FT /note= "Zins4, Claimed in claim 4"
FT Region 26..52
FT /label= B_chain
FT /note= "Claimed in claim 1"
FT Region 34..47
FT /label= B_chain_consensus_sequence_region
FT /note= "Given in SEQ ID NO 3"
FT Region 37..41
FT /label= B_chain_conserved_motif

FT Cleavage-site /note= "Given in SEQ ID NO 5"
 FT Region 53..54
 FT /label= C_peptide
 FT Region 55..118
 FT /label= C_peptide
 FT Region 55..114
 FT /label= C_peptide
 FT Cleavage-site /note= "Claimed in claim 3"
 FT 115..118
 FT /note= "Cleavage site at the junction of the C peptide
 FT and the A chain with a conserved RXR motif"
 FT Region 119..142
 FT /label= A_chain
 FT /note= "Claimed in claim 2"
 FT Region 128..142
 FT /label= A_chain_consensus_sequence_region
 FT /note= "Given in SEQ ID NO 4"
 XX
 XX WO200168862-A1.
 XX
 XX 20-SEP-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04199.
 XX
 XX 10-MAR-2000; 2000US-0523346.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Holloway JL, Lok S, Jaspers SR;
 XX
 XX WPI; 2001-582454/65.
 XX
 XX N-PSDB; AAH79088.
 XX
 XX New insulin homologue polypeptide having homology to relaxin family,
 XX designated zins4 and zins4 polynucleotide, useful for diagnosing,
 XX preventing, treating reproductive, prostate, heart and kidney disorders
 XX
 XX Claim 6; Page 72-73; 79pp; English.
 XX
 XX The invention relates to an isolated insulin homologue zins4 having
 XX homology to the relaxin family. The zins4 gene, located on chromosome
 XX 19p13.11, encodes a 142 amino acid protein, where the zins4 polypeptide
 XX comprises a B chain and A chain comprising amino acid residues 26-52 and
 XX 119-142 respectively, joined by inter- and intra-chain disulfide bonds.
 XX zins4 has cytostatic, antifertility and vasotropic activity. Zins4
 XX proteins are useful in applications for enhancing fertilisation during
 XX assisted reproduction in humans and animals and in therapies for treating
 XX reproductive disorders. Zins4 protein is useful in treating reproductive,
 XX prostate, heart or kidney disorders and to identify cells, tissues or
 XX cell lines which respond to the zins4-stimulated pathway and to identify
 XX inhibitors of its activity. Zins4 polypeptides and modulators of the
 XX polypeptide are useful in treating disorders associated with gonadal
 XX development, pregnancy, pubertal changes, menopause, ovarian cancer,
 XX prostate, testicular cancer, fertility, ovarian function, ovulation,
 XX polycystic ovarian syndrome and other reproductive functions including
 XX pathological conditions in ovary. Detection of zins4 polypeptides in the
 XX serum or tissue biopsy of a patient is useful for diagnosing ovarian
 XX cancer. The molecules are also useful for treating dysfunction associated
 XX with contractile tissues or to suppress or enhance contractility in vivo,
 XX treating cardiovascular disease, infertility, in vitro fertilization,
 XX birth control, treating impotence or other male reproductive dysfunction,
 XX inducing birth, for promoting growth, differentiation, development and/or
 XX maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in
 XX culture and in the study of the ovarian cycle, reproductive function,
 XX ovarian cell-cell interactions and fertilisation. The polypeptide is also
 XX useful as a modulator of blood pressure, muscle tension and osmotic
 XX balance. The zins4 polynucleotide is useful in gene therapy.

Sequence 142 AA;

Query Match 100.0%; Score 150; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6.3e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27
 DB 26 raapvgrlcrefiraviftcggsrw 52
 |||||

RESULT 2
 AAR96006
 ID AAR96006 standard; peptide; 40 AA.

XX AAR96006;
 AC AAR96006;
 DT 19-FEB-1997 (first entry)
 DE Asymmetry sequence #8.
 DE Asymmetry sequence #8.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
 KW virus.

OS Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US15944.

XX 09-DEC-1994; 94US-0353476.

XX (GENE-) GENE POOL INC.

XX Weininger AM, Weininger S;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection
 PT and localisation of specific nucleic acid sequences, esp. HIV and
 PT HPV

XX Claim 21; Page 108-109; 172pp; English.

XX AAR95999-R96006 represent the asymmetry sequences of target binding
 CC assemblies (TBA) of the invention. The TBA is recognised by the target
 CC binding region (TBR) of a probe of the invention. The probe of the
 CC invention contains a TBR, a booster binding region (BBR), and an
 CC optional support or attachment (OSA). The TBA contains at least one
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
 CC assembly sequence, an asymmetry sequence, a nuclear localisation signal
 CC sequence, and an OSA. The assembly sequence and asymmetry sequences are
 CC responsible for the folding and association of the NARs. The NARs are
 CC selected from NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV
 CC LTR, human immunodeficiency virus (HIV) LTR and Tat binding units.
 CC linker sequence is an oligopeptide, which does not interfere with NAR
 CC function, but provides stability and control over the spacing of the NAR
 CC from the rest of the TBA. The OSA is an attached support or indicator,
 CC or other means of localisation of the probe. The probe can be used in a
 CC method for detecting or localising a specific target nucleic acid
 CC of specificity. The method is highly sensitive, and has a high degree
 CC of specificity. The method can be used for detecting specific nucleic
 CC acid sequences, including those found in human cells, in HIV, HPV, and
 CC other nucleic acid containing systems, including bacteria and viruses.

Sequence 40 AA;

Query Match 58.0%; Score 87; DB 17; Length 40;
 Best Local Similarity 70.0%; Pred. No. 1.9e-05;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27

Db 9 rlcgrdlirafylcggrtw 28
||||| :||| : |||||

RESULT 3
AAV01963
ID AAV01963 standard; Peptide; 30 AA.

XX AC AAV01963;
XX DT 01-JUL-1999 (first entry)
XX DE Insulin-like peptide (pro-ILP) chain B peptide.
XX KW Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
KW A chain; B chain; C chain; neurophysiological function;
KW fluid homeostasis; electrolyte homeostasis; cardiovascular function;
KW blood pressure; somatic; cardiac ionotropic activity;
KW cardiac chronotropic activity; collagen deposition.
XX OS Homo sapiens.
XX PN WO9915664-A1.
XX PD 01-APR-1999.
XX PF 28-AUG-1998; 98WO-US17888.
XX PR 24-SEP-1997; 97US-0059836.
XX PS (GETH) GENENTECH INC.
XX PI Gurney A;
XX DR WPI; 1999-254713/21.
XX N-PSDB; AAX35207.
XX PT Colon and uterus expressed insulin-like polypeptide, useful in the
PT treatment of disorders related to neurophysiological function
XX PS Claim 7; Page -; 75pp; English.
XX CC The present sequence represents insulin-like polypeptide (pro-ILP)
CC chain B peptide. The ILP protein is expressed in the colon and uterus,
CC and is a member of the insulin/IGF family. The immature pro-ILP
CC comprises a 135 amino acid sequence, which is processed into the mature
CC form which comprises an A chain and a B chain linked by disulfide bonds.
CC The C-peptide of pro-ILP exists as a separate peptide after processing
CC of pro-ILP. The ILP protein is useful in treatment of disorders related
CC to neurophysiological function affecting fluid homeostasis, electrolyte
CC homeostasis, cardiovascular function, blood pressure, somatic or cardiac
CC ionotropic activity, cardiac chronotropic activity and collagen
CC deposition. The methods can be used for diagnosing a physiologic or
CC pathologic condition of the uterus, colon or other ILP-expressing cell
CC or tissue and for diagnosis and screening of modulators and therapeutics.
CC note: the present sequence does not appear in the specification; it was
CC created using information provided.
XX SQ Sequence 30 AA;

Query Match 54.7%; Score 82; DB 20; Length 30;
Best Local Similarity 66.7%; Pred. No. 7.5e-05;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
||||| :||| : |||||
Db 8 vrlcgleyirtviycassrw 28

RESULT 4
AAV95773
ID AAV95773 standard; Peptide; 31 AA.

XX AC AAY95773;
XX DT 07-NOV-2000 (first entry)
XX DE Human zins3 B chain peptide immunogen.
XX KW zins3; insulin; relaxin; human; diagnosis; NIIDM;
KW non-insulin dependent diabetes mellitus; immunogen.
XX OS Homo sapiens.
XX PN WO200047776-A2.
XX PD 17-AUG-2000.
XX PF 10-FEB-2000; 2000WO-US03515.
XX PR 12-FEB-1999; 99US-0198248.
XX PR 12-FEB-1999; 99US-0250125.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
XX WPI; 2000-558220/51.
XX DR Identifying mutations in human chromosome lp31, preferably a zins3 gene
XX PT mutation, comprises using an insulin/relaxin family member (designated
XX PT zins3), useful for diagnosing non-insulin dependent diabetes -
XX PS Example 5; Page 34; 51pp; English.
XX CC The present sequence is that of a peptide from the B chain of
CC human zins3 (see AAY95770). The peptide was used to immunize guinea
CC pigs, rabbits and chickens to generate antibodies for zins3, which
CC were used in assays to determine the tissue distribution and cell
CC expression of zins3. zins3 is a novel member of the insulin/relaxin
CC family whose gene maps to a region of human chromosome lp associated
CC with non-insulin dependent diabetes mellitus (NIDDM). zins3
CC polynucleotides and polypeptides can be used to diagnose disorders
CC associated with abnormal expression of zins3, and to identify
CC polymorphisms that result from mutations in the zins3 gene. The
CC invention provides methods for identifying abnormalities in
CC expression that are a factor in causing, or predisposing, a person
CC to some defect in glucose metabolism, such as NIDDM.
XX SQ Sequence 31 AA;

Query Match 54.7%; Score 82; DB 21; Length 31;
Best Local Similarity 66.7%; Pred. No. 7.8e-05;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
||||| :||| : |||||
Db 8 vrlcgleyirtviycassrw 28

RESULT 5
AAW37925
ID AAW37925 standard; Protein; 135 AA.

XX AC AAW37925;
XX DT 01-SEP-1998 (first entry)
XX DE Human zins3 protein.
XX KW Insulin homologue; identification; isolation; zins3 receptor;
KW treatment; disease; pre-elapsia; premature labour; Human.
XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 23..48 "B chain"
 FT /note="B chain"
 FT Peptide 49..114
 FT /note="C-peptide"
 FT Peptide 115..135
 FT /note="A chain"
 XX WO9816635-A1.
 PN 23-APR-1998.
 XX 15-OCT-1997; 97WO-US18593.
 XX 15-OCT-1996; 96US-0028177.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Conklin DC, Jaspers SR, Lofton-Day CE, Lok S;
 PI WPI; 1998-251285/22.
 XX N-PSDB; AAV29150.
 XX Insulin homologue polypeptide(s) and antagonists - used to, e.g.
 XX treat pre-eclampsia, premature labour and Crohn's disease.
 XX Claim 2; Page 64-65; 81pp; English.
 XX The zins3 protein is an insulin homologue protein. Polynucleotide
 CC molecules taken from its gene can be introduced into a cultured cell
 CC using an expression vector. The cell will express an insulin homologue
 CC polypeptide encoded by the polynucleotide. The polypeptides can also be
 CC expressed by introducing the polynucleotides into the germline of a
 CC nonhuman animal. The polypeptides can be used to identify and isolate
 CC receptors for zins3. Antibodies and antagonists of the polypeptides can
 CC be used for treating disease associated with extracellular matrix and
 CC vessels. The antibodies may also be used in the diagnosis of diseases
 CC associated with the polypeptide, such as reproductive disorders
 CC associated with the placenta and uterus, gastrointestinal diseases, and
 CC placental and colon pathology. Antagonists against the polypeptide may
 CC also be used to treat diseases such as preclampsia, premature labour, and
 CC Crohn's disease.
 XX Sequence 135 AA;
 SQ

Query Match 54.7%; Score 82; DB 19; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 7 VRLCGREFIRAVFTCGGSRW 27
 DB 26 vrlcgleiyrtviycasrw 46

RESULT 6
 AAY01961
 ID AAY01961 standard; Protein; 135 AA.
 XX
 AC AAY01961;
 XX 01-JUL-1999 (first entry)
 XX
 DE Pro-insulin-like peptide (pro-ILP).
 XX Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family;
 KW A chain; B chain; C chain; neurophysiological function;
 KW fluid homeostasis; electrolyte homeostasis; cardiovascular function;
 KW blood pressure; somatic; cardiac ionotropic activity;
 KW cardiac chronotropic activity; collagen deposition.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT /Label= Signal peptide
 FT Modified-site 3..9
 FT /note= "N-myristoylation site"
 FT Modified-site 52..58
 FT /note= "N-myristoylation site"
 FT

XX WO9915664-A1.
 XX 01-APR-1999.
 XX 28-AUG-1998; 98WO-US17888.
 XX 24-SEP-1997; 97US-0059836.
 XX (GETH) GENENTECH INC.
 XX Gurney A;
 PI WPI; 1999-254713/21.
 XX N-PSDB; AAX35204.
 XX Colon and uterus expressed insulin-like polypeptide, useful in the
 XX treatment of disorders related to neurophysiological function
 XX Claim 5; Fig 6B; 75pp; English.
 XX The present sequence represents an insulin-like polypeptide (pro-ILP).
 CC The protein is expressed in the colon and uterus, and is a member
 CC of the insulin/IGF family. The immature pro-ILP comprises a 135 amino
 CC acid sequence, which is processed into the mature form which comprises
 CC an A chain and a B chain linked by disulfide bonds. The C-peptide of
 CC pro-ILP exists as a separate peptide after processing of pro-ILP. The
 CC ILP protein is useful in treatment of disorders related to
 CC neurophysiological function affecting fluid homeostasis, electrolyte
 CC homeostasis, cardiovascular function, blood pressure, somatic or cardiac
 CC ionotropic activity, cardiac chronotropic activity and collagen
 CC deposition. The methods can be used for diagnosing a physiologic or
 CC pathologic condition of the uterus, colon or other ILP-expressing cell
 CC or tissue and for diagnosis and screening of modulators and therapeutics.
 XX Sequence 135 AA;
 SQ

Query Match 54.7%; Score 82; DB 20; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 7 VRLCGREFIRAVFTCGGSRW 27
 DB 26 vrlcgleiyrtviycasrw 46

RESULT 7
 AAB00173
 ID AAB00173 standard; Protein; 135 AA.
 XX
 AC AAB00173;
 XX 08-FEB-2001 (first entry)
 XX PRO182 polypeptide.
 XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition;
 KW tumour; treatment; therapy; agonist; antibody; breast cancer;
 KW ovarian cancer; renal cancer; colorectal cancer; uterine cancer;
 KW prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia;
 KW inflammatory disorder; angiogenic disorder; immunologic disorder;
 KW human.
 XX Homo sapiens.
 OS

FT Modified-site 88..92 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 96..102 /note= "N-myristoylation site"
 FT Modified-site 107..111 /note= "cAMP- and cGMP-dependent protein kinase"
 FT Modified-site 113..117 /note= "Casein kinase II phosphorylation site"
 FT Domain 121..136 /label= Insulin family signature
 FT Modified-site 125..131 /note= "N-myristoylation site"
 FT Modified-site 127..131 /note= "Casein kinase II phosphorylation site"
 XX
 PN WO200055319-A1.
 XX
 PN 21-SEP-2000.
 PD
 PD 02-DEC-1999; 99WO-US28564.
 XX
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WT;
 PI Yuan J;
 XX WPI; 2000-638201/61.
 DR N-PSDB; AAA54109.
 XX
 XX PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
 PT treating tumors including cancers of the breast and lung,
 PT leukemia and for identifying compounds capable of inhibiting
 PT growth of neoplastic cells
 XX
 PS Claim 31; Fig 10; 133pp; English.
 XX
 CC Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides
 CC or their agonists (preferably anti-PRO agonist antibody or a small
 CC molecule mimicking the biological activity of PRO polypeptide) are
 CC useful in vitro or in vivo for inhibiting the growth of a tumour cell.
 CC Compositions comprising the PRO polypeptides are useful for
 CC inhibiting neoplastic cell growth and for treating cancer including
 CC breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,
 CC central nervous system cancer, melanoma and leukemia in a mammal.
 CC The PRO polypeptides are also useful for treating other disorders
 CC such as neuronal, glial, astrocytal, hypothalamic and other glandular,
 CC macrophagal, epithelial, stromal, blastocoelec disorders and
 CC inflammatory, angiogenic and immunologic disorders as well as being
 CC useful for identifying agonists to PRO polypeptides by contacting the
 CC polypeptide with a candidate molecule and monitoring biological
 CC activity mediated by the polypeptide.
 XX
 SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVITTCGSRW 27
 ||||| I:|:| | | | | | | |
 Db 26 vrlcglevrtviycassrw 46

RESULT 8
 AAB24391
 ID AAB24391 standard; Protein; 135 AA.
 XX
 AC AAB24391;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human PRO182 protein sequence SEQ ID NO:16.
 XX
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytosstatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200032221-A2.
 XX
 PD 08-JUN-2000.
 XX
 PD 30-NOV-1999; 99WO-US28313.
 XX
 PR 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 12-JAN-1999; 99US-0115554.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
 PI Watanabe CK, Williams PM, Wood WT;
 XX
 DR WPI; 2000-412154/35.
 DR N-PSDB; AAA77521.
 XX
 XX Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating polypeptides a cardiovascular, endothelial or
 PT angiogenic disorders in mammals -
 XX
 PS Claim 72; Fig 8; 315pp; English.
 XX
 XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 135 AA;

members of the insulin family, cleavage at the C-terminus of the B-chain and at the N-terminus of the A-chain, resulting in removal of the C-peptide. Cysteine residues at positions 29 and 41 (B-chain) and 121 and 135 (A-chain) are capable of associating through cysteine bridges and forming disulfide-bonded molecules.

Qv 7 VRLCGREEIRAVIETCGGSRW 27

DD 26 vricgleylrvtvlyicassiw 46
 RESULT 9
 AAY95770
 ID AAY95770 standard; Protein: 135 AA.

Query Match 54.7%; Score 82; DB 21; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14: Conservative 2; Mismatches 5; Indels

| | | | |
|----|----|------------------------|----|
| QY | 7 | VRLCGREFIRAVIFTCGSRW | 27 |
| | | 1: 1: 1 | |
| pb | 26 | vrclalevtrtvi vicassrw | 46 |

DT 07-NOV-2000 (first entry)

XX

DE Human ins

XX

XX Composition for inhibiting neoplastic cell growth and treating cancers
PT of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
PT PRO538, PRO172 or PRO182 polypeptide or their agonist
XX

PS Claim 14; Figure 10; 122pp; English.

XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
CC polypeptide or their agonists, mixed with a carrier is useful for
CC inhibiting neoplastic growth and treating tumors such as cancers of
CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
CC central nervous system, melanoma and leukaemia.
XX

SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 21; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
||||| I:|:| I:|:| I:|:|
Db 26 vrlcgleiyrtviycassrw 46

RESULT 11
AAM24033
ID AAM24033 standard; Protein; 135 AA.

AC AAM24033;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1558.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.

PN WO200154477-A2.

XX 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02687.

PR 25-JAN-2000; 2000US-0491404.

PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

PR 15-SEP-2000; 2000US-0663870.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;

DR WPI; 2001-476164/51.

XX N-PSDB; AAH98692.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -

PS Claim 20; Page 1068-1069; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention.
XX
SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
Best Local Similarity 66.7%; Pred. No. 0.00034;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
||||| I:|:| I:|:| I:|:|
Db 26 vrlcgleiyrtviycassrw 46

RESULT 12

AAU12309

ID AAU12309 standard; Protein; 135 AA.

AC AAU12309;

DT 24-OCT-2001 (first entry)

XX Human PRO182 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.

PN WO200140466-A2.

XX 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31243.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 01-MAR-2000; 2000WO-US05601.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 10-NOV-2000; 2000WO-US30873.

XX (GETH) GENENTECH INC.

PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21381.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 276; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 ||||| I:|:| | | |
 Db 26 vrlcgleyirtviycassrw 46

RESULT 13
 AAB20110
 ID AAB20110 standard; Protein; 135 AA.
 AC AAB20110;
 XX
 XX 30-APR-2001 (first entry)
 XX
 DE Human immunostimulant PRO182.
 XX
 KW PRO182; UNQ156; human; immune disease; autoimmune disease;
 KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
 KW hepatotropic; virucide; dermatological; antipsoriatic;
 KW antiaschmatic; anti allergic; immunostimulant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Signal_peptide
 FT 19..135
 FT /label= Mature_protein
 FT 107..111
 FT Modified-site /note= "cAMP- and cGMP-dependent protein kinase
 FT phosphorylation site"
 FT
 FT Modified-site 3..9
 FT /note= "N-myristoylation site"
 FT
 FT Modified-site 52..58
 FT /note= "N-myristoylation site"
 FT
 FT Modified-site 96..102
 FT /note= "N-myristoylation site"

FT Modified-site 125..131
 FT /note= "N-myristoylation site"
 FT Peptide 121..136
 FT /note= "insulin family signature"
 XX
 PN WO200105972-A1.
 XX
 PD 25-JAN-2001.
 XX
 XX 15-MAR-2000; 2000WO-US06884.
 PF
 XX 20-JUL-1999; 99US-0144758.
 PR
 XX (GETH) GENENTECH INC.
 PA
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;
 PI Wood WI;
 XX
 DR WPI; 2001-103149/11.
 DR N-PSDB; AAF30052.
 XX
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
 PT diagnosing and treating immune-related disorders, such as multiple
 PT sclerosis, rheumatoid arthritis and diabetes -
 XX
 PS Claim 20; Fig 6; 127pp; English.
 XX
 CC The present sequence is that of PRO182 (UNQ156), a novel human
 CC immunomodulator protein encoded by cDNA (see AAF30052) isolated
 CC from a uterine cDNA library. The invention provides polynucleotides
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
 CC including PRO182. Claimed compositions comprising these proteins or
 CC their agonists are useful for increasing infiltration of inflammatory
 CC cells into a tissue of a mammal, stimulating or enhancing an immune
 CC response in a mammal, or increasing the proliferation of T-lymphocytes
 CC in a mammal in response to an antigen. Claimed compositions
 CC comprising the PRO polypeptide or its antagonist have the opposite
 CC effect. A claimed method for treating an immune related disorder,
 CC such as a T cell disorder, involves administering the PRO polypeptide,
 CC an agonist antibody or an antagonist antibody. The disorder is
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathy,
 CC systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinated diseases (such as
 CC multiple sclerosis), autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),
 CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated
 CC skin diseases (such as bullous skin disease, erythema multiforme and
 CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,
 CC atopic dermatitis, food hypersensitivity and urticaria), immunologic
 CC diseases of the lung and transplantation associated diseases (such
 CC as graft rejection and graft-versus-host disease) (all claimed).
 CC Claimed methods of diagnosing these disorders comprise detecting
 CC the level of expression of the PRO gene. Also claimed are a method
 CC of identifying a compound capable of inhibiting the expression or
 CC activity of the PRO polypeptide, vectors, host cells and
 CC antibodies.
 XX
 SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;
 Best Local Similarity 66.7%; Pred. No. 0.00034;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 ||||| I:|:| | | |
 Db 26 vrlcgleyirtviycassrw 46

RESULT 14

AAB53072

ID AAB53072 standard; Protein; 135 AA.

AC AAB53072;

XX

DT 28-FEB-2001 (first entry)

XX

DE Human angiogenesis-associated protein PRO182, SEQ ID NO:41.

XX

KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.

XX

OS Homo sapiens.

XX

PN WO200053753-A2.

XX

PD 14-SEP-2000.

XX

PF 05-JAN-2000; 2000WO-US00219.

XX

PR 08-MAR-1999; 99WO-US05028.

PR

PR 12-MAR-1999; 99US-0123957.

PR

PR 14-MAY-1999; 99US-0134287.

PR

PR 02-JUN-1999; 99WO-US12252.

PR

PR 23-JUN-1999; 99US-0141037.

PR

PR 20-JUL-1999; 99US-0144758.

PR

PR 26-JUL-1999; 99US-0145698.

PR

PR 01-SEP-1999; 99WO-US20111.

PR

PR 08-SEP-1999; 99WO-US20534.

PR

PR 15-SEP-1999; 99WO-US21090.

PR

PR 15-SEP-1999; 99WO-US21547.

PR

PR 05-OCT-1999; 99WO-US23089.

PR

PR 30-NOV-1999; 99WO-US28313.

PR

PR 30-NOV-1999; 99WO-US28409.

PR

PR 02-DEC-1999; 99WO-US28564.

PR

PR 02-DEC-1999; 99WO-US28565.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Ferrata N, Gerber H, Goddard A;

PI

PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

PI

XX Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX

DR WPI; 2001-090793/10.

DR

DR N-PSDB; AAC97396.

XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX

PS

XX Claim 69; Fig 18; 293pp; English.

XX

CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a PRO protein of the
 CC invention.

SQ Sequence 135 AA;

Query Match 54.7%; Score 82; DB 22; Length 135;

Best Local Similarity 66.7%; Pred. No. 0.00034;

Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVITCGSRW 27

|||||:|:|:|:|:|

Db 26 vrlcgleiyftviycassrw 46

RESULT 15

AABW07863

ID AABW07863 standard; peptide; 31 AA.

AC AABW07863;

XX

DT 27-AUG-1997 (first entry)

XX

DE Relaxin-like factor B chain.

XX

KW A chain; B chain; relaxin-like factor; RLF; relaxin;

KW cardiovascular disease; neurodegenerative disease;

KW neurological disease; sinus bradycardia; depression; hair loss;

KW collagen; scleroderma; fibronectin; insulin.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 10

FT /note= "Forms disulphide bond with A chain Cys11"

FT Disulfide-bond 22

FT /note= "Forms disulphide bond with A chain Cys24"

XX

PN WO9640186-A1.

XX

XX 19-DEC-1996.

XX

XX 16-MAY-1996; 96WO-US07399.

XX

XX 07-JUN-1995; 95US-0484219.

XX

XX (CONN-) CONNECTIVE THERAPEUTICS INC.

XX (UYSC-) UNIV SOUTH CAROLINA.

XX

XX Schwabe C, Unemori E;

XX

XX WPI; 1997-051882/05.

XX

PT Relaxin-like factor - useful as replacement for relaxin in treatment
 PT of, e.g. cardiovascular or neurodegenerative disease

XX

PS Claim 1; Page 48; 60pp; English.

XX

CC The sequences given in AAW07862-63 represent the A and B chains of
 CC relaxin-like factor (RLF). RLF displaces bound relaxin tracer from
 CC the receptor to which it is bound. The RLF can be used to treat
 CC relaxin treatable conditions, esp. cardiovascular disease, neuro-
 CC degenerative or neurological disease, sinus bradycardia, depression,
 CC hair loss or diseases related to uncontrolled or abnormal formation of
 CC collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled
 CC for use in binding assays, and for relaxin receptor mapping. RLF
 CC shares primary and secondary homology to relaxin and insulin.

XX
 SQ Sequence 31 AA;

Query Match 50.7%; Score 76; DB 18; Length 31;
 Best Local Similarity 55.0%; Pred. No. 0.00056;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGRFIRAVIFTCGSRW 27
 :||| |::|:: ||| ||
 Db 8 klcghivralrvvcgprw 27

Search completed: June 27, 2002, 16:08:09
 Job time: 278 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:08:44 ; Search time 28.78 Seconds
(without alignments)
22.915 Million cell updates/sec

Title: US-09-781-077-2_COPY_26_52

Perfect score: 150
Sequence: 1 RAAPYGVRLCGREFIRAVITCGSRW 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 116 | 77.3 | 30 | 6 | Patent No. 5464756 |
| 2 | 102 | 68.0 | 29 | 6 | Patent No. 5464756 |
| 3 | 87 | 58.0 | 40 | 2 | Sequence 92, Appl |
| 4 | 82 | 54.7 | 135 | 3 | Sequence 2, Appl |
| 5 | 76 | 50.7 | 31 | 2 | Sequence 4, Appl |
| 6 | 76 | 50.7 | 101 | 3 | Sequence 14, Appl |
| 7 | 75 | 50.0 | 135 | 3 | Sequence 6, Appl |
| 8 | 71 | 47.3 | 29 | 1 | Sequence 2, Appl |
| 9 | 71 | 47.3 | 29 | 2 | Sequence 5, Appl |
| 10 | 71 | 47.3 | 29 | 5 | Sequence 2, Appl |
| 11 | 71 | 47.3 | 32 | 6 | Sequence 5, Appl |
| 12 | 71 | 47.3 | 33 | 6 | Sequence 2, Appl |
| 13 | 71 | 47.3 | 52 | 1 | Patent No. 5464756 |
| 14 | 71 | 47.3 | 52 | 5 | Sequence 14, Appl |
| 15 | 71 | 47.3 | 77 | 1 | Sequence 10, Appl |
| 16 | 71 | 47.3 | 77 | 5 | Sequence 10, Appl |
| 17 | 71 | 47.3 | 162 | 6 | Patent No. 5464756 |
| 18 | 71 | 47.3 | 164 | 6 | Patent No. 5464756 |
| 19 | 71 | 47.3 | 185 | 3 | Sequence 12, Appl |
| 20 | 71 | 47.3 | 185 | 3 | Sequence 13, Appl |
| 21 | 69 | 46.0 | 33 | 2 | Sequence 90, Appl |
| 22 | 68 | 45.3 | 29 | 2 | Sequence 1, Appl |
| 23 | 68 | 45.3 | 29 | 4 | Sequence 1, Appl |
| 24 | 67 | 44.7 | 35 | 6 | Patent No. 5464756 |
| 25 | 57 | 38.0 | 32 | 6 | Patent No. 5464756 |
| 26 | 55 | 36.7 | 32 | 6 | Patent No. 5464756 |
| 27 | 53 | 35.3 | 150 | 1 | Sequence 12, Appl |

28 53 35.3 150 5 PCT-US94-06997-12 Sequence 12, Appl
29 53 35.3 188 2 US-08-905-267-2 Sequence 2, Appl
30 53 35.3 188 4 US-09-314-051-2 Sequence 2, Appl
31 51 34.0 35 6 5464756-13 Patent No. 5464756
32 49 32.7 213 2 US-08-905-267-13 Sequence 13, Appl
33 49 32.7 213 4 US-09-314-051-13 Sequence 23, Appl
34 48 32.0 603 4 US-09-097-889-23 Patent No. 5352575
35 47.5 31.7 577 6 5352575-9 Patent No. 5470721
36 47 31.3 29 1 US-08-435-252-1 Patent No. 5470721
37 47 31.3 33 6 5470721-2 Patent No. 5489517
38 47 31.3 36 6 5489517-2 Patent No. 5489517
39 47 31.3 50 6 5436136-16 Patent No. 5436136
40 47 31.3 67 4 US-07-963-329A-2 Sequence 2, Appl
41 47 31.3 67 5 PCT-US92-09443A-2 Sequence 2, Appl
42 47 31.3 70 1 US-07-654-611-2 Sequence 2, Appl
43 47 31.3 70 1 US-08-180-572-5 Sequence 5, Appl
44 47 31.3 70 1 US-07-947-035-1 Sequence 1, Appl
45 47 31.3 70 1 US-07-776-272-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
5464756-16
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA: US/07/908,766
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:16:
; LENGTH: 30
5464756-16

Query Match 77.3%; Score 116; DB 6; Length 30;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 GVRLCGREFIRAVITCGSRW 27
Db 9 GIRLCGREFIRAVITCGSRW 30
:::|||||:::|||||

RESULT 2
5464756-15
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:15:
; LENGTH: 29
5464756-15

Query Match 68.0%; Score 102; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 1.7e-08;
Matches 17; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GVRLCGREFIRAVFTCGGSRW 26
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 9 GIKLCGREFIRAVFTACGGSRW 29

RESULT 3

US-08-353-476-92
 ; Sequence 92, Application US/08353476
 ; Patent No. 5871902
 ; GENERAL INFORMATION:
 ; APPLICANT: Weininger, Susan
 ; APPLICANT: Weininger, Arthur M
 ; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
 ; NUMBER OF SEQUENCES: 117
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st St., Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/353,476
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Benzen, Gerard H
 ; REGISTRATION NUMBER: 35,746
 ; REFERENCE/DOCKET NUMBER: GP-100
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (904) 375-8100
 ; TELEFAX: (904) 372-5800
 ; INFORMATION FOR SEQ ID NO: 92:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; US-08-353-476-92

Query Match 58.0%; Score 87; DB 2; Length 40;
 Best Local Similarity 70.0%; Pred. No. 3.6e-06;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 9 RLCGRDLIRAVFTLCGGTRW 28

RESULT 4

US-08-950-720A-2
 ; Sequence 2, Application US/08950720A
 ; Patent No. 6046028
 ; GENERAL INFORMATION:
 ; APPLICANT: Conklin, Darrell C.
 ; APPLICANT: Lofton-Day, Catherine E.
 ; APPLICANT: Lok, Si
 ; APPLICANT: Jaspers, Stephen R.
 ; TITLE OF INVENTION: INSULIN HOMOLOG
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/950,720A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sawislak, Deborah A
 ; REGISTRATION NUMBER: 37,438
 ; REFERENCE/DOCKET NUMBER: 96-09
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6672
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 135 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-950-720A-2

Query Match 54.7%; Score 82; DB 3; Length 135;
 Best Local Similarity 66.7%; Pred. No. 6.5e-05;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 I:|||||I:|||||I:|||||I:|||||I:|||||
 Db 26 VRLCGLEYIRTVIYCASSRW 46

RESULT 5

US-08-484-219-4
 ; Sequence 4, Application US/08484219
 ; Patent No. 5911997
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwabe, Christian
 ; APPLICANT: Unemori, Elaine
 ; TITLE OF INVENTION: RELAXIN-LIKE FACTOR AND METHODS AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,219
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-040
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-219-4

Query Match 50.7%; Score 76; DB 2; Length 31;
Best Local Similarity 55.0%; Pred. No. 0.00011;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 8 KLCGHFVRALVRVCGGPRW 27

RESULT 6
US-08-950-720A-14
; Sequence 14, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
US-08-950-720A-14

Query Match 50.7%; Score 76; DB 3; Length 101;
Best Local Similarity 55.0%; Pred. No. 0.00036;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 32 KLCGHFVRALVRVCGGPRW 51

RESULT 7
US-08-950-720A-6
; Sequence 6, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-950-720A-6

Query Match 50.0%; Score 75; DB 3; Length 135;
Best Local Similarity 52.4%; Pred. No. 0.00068;
Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
:|||||:|||||
Db 26 VKLCGLDYVRTVIICASSRW 46

RESULT 8
US-08-443-568B-2
; Sequence 2, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim

```

; APPLICANT: Havenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-443-568B-2

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```

Query Match 47.3%; Score 71; DB 1; Length 29;
Best Local Similarity 57.1%; Pred. NO. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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```

QY 7 VRLCGREFIRAVITCGGSRW 27
   ::|||::|||::|||
Db 8 IKLCGRELVRQAICGMSTW 28

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RESULT 9
; Sequence 5, Application US/08484219
; Patent No. 5911997
; GENERAL INFORMATION:
; APPLICANT: Schwabe, Christian
; APPLICANT: Unemori, Elaine
; TITLE OF INVENTION: RELAXIN-LIKE FACTOR AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,219
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7842-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-219-5

```

```

Query Match 47.3%; Score 71; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. NO. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 7 VRLCGREFIRAVITCGGSRW 27
   ::|||::|||::|||
Db 8 IKLCGRELVRQAICGMSTW 28

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```

RESULT 10
; Sequence 2, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06997
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7842-025-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown

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; MOLECULE TYPE: protein
PCT-US94-06997-2

Query Match 47.3%; Score 71; DB 5; Length 29;
Best Local Similarity 57.1%; Pred. No. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 8 IKLCGRELVRQAICGMSTW 28

RESULT 11

5464756-11
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:11:
; LENGTH: 32
5464756-11

Query Match 47.3%; Score 71; DB 6; Length 32;
Best Local Similarity 57.1%; Pred. No. 0.00062;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 7 IKLCGRELVRQAICGMSTW 27

RESULT 12

5464756-10
; Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
; JAMES A.; YANSURA, DANIEL G.
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
; ISOLATION HUMAN RELAXIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,766
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO:10:
; LENGTH: 33
5464756-10

Query Match 47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 8 IKLCGRELVRQAICGMSTW 28

RESULT 13

US-08-443-568B-14
; Sequence 14, Application US/08443568B
; Patent No. 5759807

; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-443-568B-14

Query Match 47.3%; Score 71; DB 1; Length 52;
Best Local Similarity 57.1%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
Db 31 IKLCGRELVRQAICGMSTW 51

RESULT 14

PCT-US94-06997-14
; Sequence 14, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06997
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7842-025-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06997-14

Query Match 47.3%; Score 71; DB 5; Length 52;
Best Local Similarity 57.1%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
DB 31 IKLCGRELVRQAIAICGMSTW 51

RESULT 15

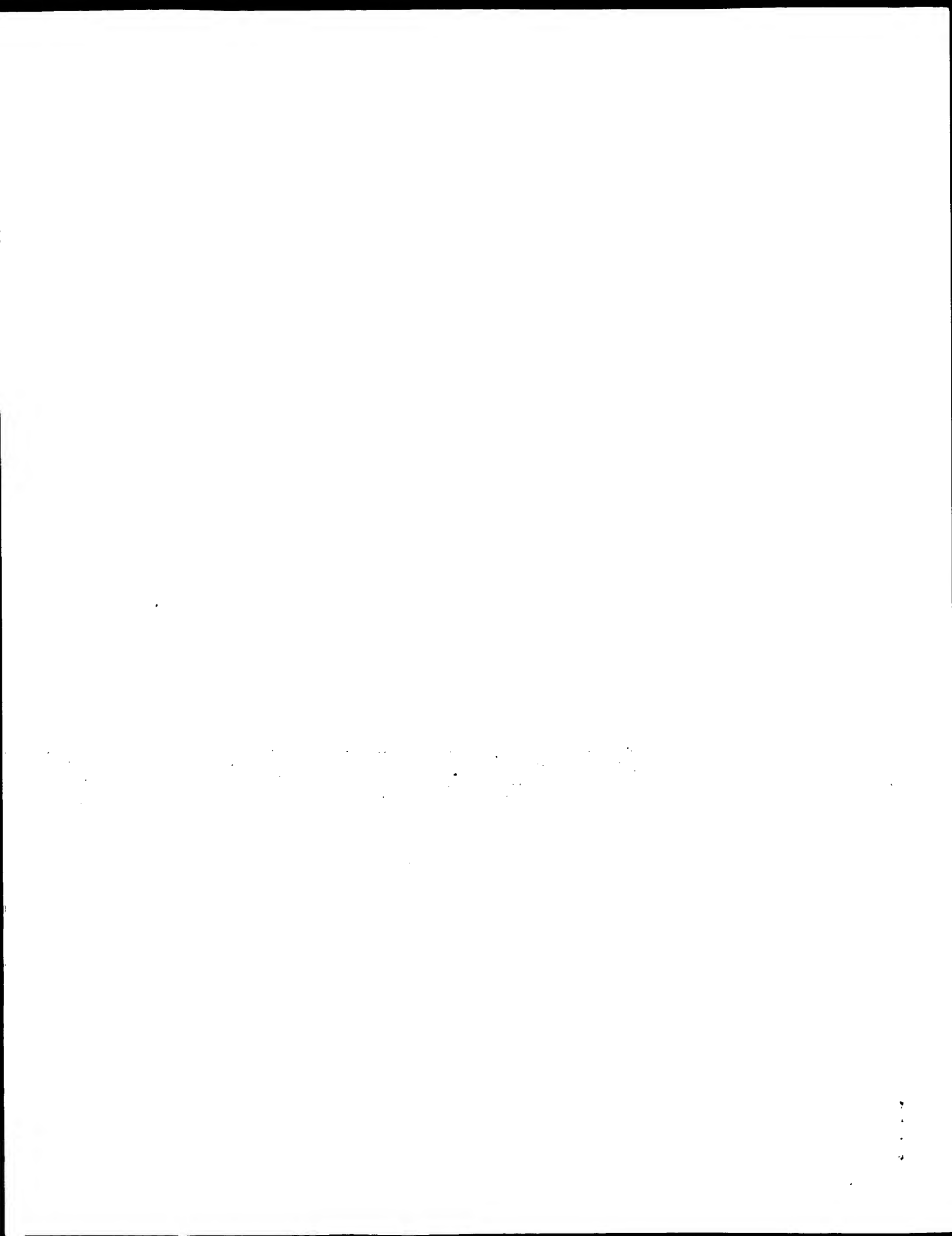
US-08-443-568B-10
; Sequence 10, Application US/08443568B
; Patent No. 5759807
; GENERAL INFORMATION:
; APPLICANT: Breece, Tim
; APPLICANT: Hayenga, Kirk
; APPLICANT: Rindersknecht, Ernst
; APPLICANT: Vandlen, Richard
; APPLICANT: Daniel, Yansura
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,568B
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,354
; FILING DATE: 21-JUNE-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adams, Samuel B.
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 7842-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-443-568B-10

Query Match 47.3%; Score 71; DB 1; Length 77;
Best Local Similarity 57.1%; Pred. No. 0.0015;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGSRW 27
DB 19 IKLCGRELVRQAIAICGMSTW 39

Search completed: June 27, 2002, 16:08:44
Job time: 193 sec



A:Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus
 A:Reference number: A91179; MUID:87054035
 A:Contents: annotation; sequence revision
 A:Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
 C:Superfamily: Insulin
 C:Keywords: pyroglutamic acid
 F:1-19/Domain: chain B (fragments) #status experimental <CHB>
 F:21-44/Domain: chain A #status experimental <CHA>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3-31,15-44,30-35/disulfide bonds: #status predicted

Query Match 64.0%; Score 96; DB 1; Length 44;
 Best Local Similarity 80.0%; Pred. No. 1.9e-07;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 1 QLCGRGTRIAIFACGGSRW 20

RESULT 3
 A29543
 relaxin - little skate (fragments)
 C:Species: Raja erinacea (little skate)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
 C:Accession: A29543
 R:Bullesbach, E.E.; Schwabe, C.; Calliard, I.P.
 Biochem. Biophys. Res. Commun. 143, 273-280, 1987
 A:Title: Relaxin from an oviparous species, the skate (Raja erinacea).
 A:Reference number: A29543; MUID:87156758
 A:Accession: A29543
 A:Molecule type: protein
 A:Residues: 1-64 <BUL>
 A:Experimental source: ovary
 C:Superfamily: insulin

Query Match 58.0%; Score 87; DB 2; Length 64;
 Best Local Similarity 70.0%; Pred. No. 5.9e-06;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 9 RLCGRDLIRAFIYLCGGTRW 28

RESULT 4
 B53024
 Leydig insulin-like protein precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: B53024; I54278
 R:Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
 Genomics 20, 13-19, 1994
 A:Title: Structural organization of the porcine and human genes coding for a Leydig cell
 A:Reference number: A53024; MUID:94292172
 A:Accession: B53024
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-131 <BUR>
 A:Cross-references: GB:X73637
 R:Burkhardt, E.; Adham, I.M.; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
 Hum. Genet. 94, 91-94, 1994
 A:Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
 A:Reference number: I54278; MUID:94307715
 A:Accession: I54278
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-131 <RES>
 A:Cross-references: GB:S72482; NID:g632798; PIDN:AAB31371.1; PID:g632799
 C:Genetics:
 A:Gene: GDB:INSL3

A:Cross-references: GDB:230307; OMIM:146738
 A:Map position: 19p13.2-19p12
 A:Introns: 64/1

Query Match 50.7%; Score 76; DB 2; Length 131;
 Best Local Similarity 55.0%; Pred. No. 0.0005;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 32 KLCGHHFVRALVRCGGPRW 51

RESULT 5
 A53024
 Leydig insulin-like protein precursor - pig
 N:Alternate names: Ley I-L
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A53024; A49687
 R:Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
 Genomics 20, 13-19, 1994
 A:Title: Structural organization of the porcine and human genes coding for a Leydig c
 A:Reference number: A53024; MUID:94292172
 A:Accession: A53024
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-131 <BUR>
 A:Cross-references: GB:X73636; NID:g871548; PIDN:CAA52016.1; PID:g871549
 R:Adham, I.M.; Burkhardt, E.; Benahmed, M.; Engel, W.
 J. Biol. Chem. 268, 26668-26672, 1993
 A:Title: Cloning of a cDNA for a novel insulin-like peptide of the testicular Leydig
 A:Reference number: A49687; MUID:94075362
 A:Accession: A49687
 A:Molecule type: mRNA
 A:Residues: 1-131 <ADH>
 A:Cross-references: GB:X58369
 A:Experimental source: testis
 A:Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
 C:Genetics:
 A:Gene: INSL3
 A:Map position: 19p13.2-pl2
 A:Introns: 64/1
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-56/Domain: Leydig insulin-like protein chain B #status predicted <BCH>
 F:57-105/Domain: connecting C peptide #status predicted <CPEP>
 F:106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>

Query Match 50.0%; Score 75; DB 2; Length 131;
 Best Local Similarity 55.0%; Pred. No. 0.0007;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVIFTCGGSRW 27
 :|||||:|||||:|||||
 Db 32 KLCGHHFVRALVRCGGPRW 51

RESULT 6
 S42786
 relaxin 2 precursor - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S42786
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42786
 A:Molecule type: mRNA
 A:Residues: 1-166 <EVA>
 A:Cross-references: EMBL:Z27245; NID:g416109; PIDN:CAA81758.1; PID:g416110
 C:Genetics:

A:Gene: rlx2
 C:Superfamily: insulin
 F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
 F:6-166/Product: relaxin 2 #status predicted <MAT>

Query Match 48.0%; Score 72; DB 2; Length 166;
 Best Local Similarity 57.1%; Pred. No. 0.0024; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 :|||||:| | | | |
 Db 13 IKLCGRELVRQAICGKSTW 33

RESULT 7
 S42784
 relaxin - gorilla (fragments)
 C:Species: Gorilla gorilla (gorilla)
 C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: S42784; S42779
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42784
 A:Molecule type: DNA
 A:Residues: 1-33 <EVA>
 A:CROSS-references: EMBL:Z27237; NID:9416010; PIDN:CAA81751.1; PID:9416011
 A:Note: chain 2B
 A:Accession: S42779
 A:Molecule type: DNA
 A:Residues: 34-57 <EVA>
 A:CROSS-references: EMBL:Z27228; NID:9415952; PIDN:CAA81742.1; PID:9415953
 A:Note: chain 2A
 C:Genetics:
 A:Gene: rlx2
 C:Superfamily: insulin
 C:Keywords: disulfide bond; hormone
 F:1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>
 F:34-57/Domain: relaxin chain 2A (fragment) #status predicted <RXA2>

Query Match 47.3%; Score 71; DB 2; Length 57;
 Best Local Similarity 57.1%; Pred. No. 0.0013; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 :|||||:| | | | |
 Db 8 IKLCGRELVRQAICGKSTW 28

RESULT 8
 S42783
 relaxin 1 precursor - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S42783
 R:Evans, B.B.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S42776
 A:Accession: S42783
 A:Molecule type: mRNA
 A:Residues: 1-166 <EVA>
 A:CROSS-references: EMBL:Z27225; NID:9415996; PIDN:CAA81739.1; PID:9415997
 C:Genetics:
 A:Gene: rlx1
 C:Superfamily: insulin
 C:Keywords: disulfide bond; hormone
 F:1-5/Domain: signal sequence (fragment) #status predicted <SIG>
 F:6-166/Product: relaxin 1 #status predicted <MAT>

Query Match 47.3%; Score 71; DB 2; Length 166;

Best Local Similarity 57.1%; Pred. No. 0.0035;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 :|||||:| | | | |
 Db 13 IKLCGRELVRQAICGKSTW 33

RESULT 9
 A44559
 relaxin 1 precursor - human
 N:Alternate names: preprorelaxin 1
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
 C:Accession: B05092; A44559
 R:Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear, E.M.B.
 EMBO J. 3, 2333-2339, 1984
 A:Title: Relaxin gene expression in human ovaries and the predicted structure of a human relaxin.
 A:Reference number: A05092; MUID:85051298
 A:Accession: B05092
 A:Molecule type: DNA
 A:Residues: 1-185 <HU1>
 A:CROSS-references: GB:X00949; NID:935932; PIDN:CAA25461.1; PID:935933
 R:Hudson, P.; Hales, J.; John, M.; Cronk, M.; Crawford, R.; Haralambidis, J.; Tregear, E.M.B.
 Nature 301, 628-631, 1983
 A:Title: Structure of a genomic clone encoding biologically active human relaxin.
 A:Reference number: A44559; MUID:83141755
 A:Accession: A44559
 A:Molecule type: DNA
 A:Residues: 1-185 <HU2>
 A:CROSS-references: GB:X00949; NID:935932; PIDN:CAA25461.1; PID:935933
 C:Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of the cervix.
 C:Genetics:
 A:Gene: GDB:RLN1
 A:CROSS-references: GDB:119552; OMIM:179730
 A:Map position: 9pter-q12
 C:Superfamily: insulin
 C:Keywords: hormone; ovary
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-57,162-185/Product: relaxin 1 chain B #status predicted <BCH>
 F:58-138/Domain: relaxin 1 connecting C peptide #status predicted <MAT>
 F:162-185/Domain: relaxin 1 chain A #status predicted <ACH>
 F:35-172,47-185,171-176/Disulfide bonds: #status predicted

Query Match 47.3%; Score 71; DB 1; Length 185;
 Best Local Similarity 57.1%; Pred. No. 0.0038; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 :|||||:| | | | |
 Db 32 IKLCGRELVRQAICGKSTW 52

RESULT 10
 A60982
 relaxin 2 precursor [validated] - human
 N:Alternate names: preprorelaxin 2
 C:Species: Homo sapiens (man)
 C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
 C:Accession: A05092; A60982
 R:Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear, E.M.B.
 EMBO J. 3, 2333-2339, 1984
 A:Title: Relaxin gene expression in human ovaries and the predicted structure of a human relaxin.
 A:Reference number: A05092; MUID:85051298
 A:Accession: A05092
 A:Molecule type: mRNA
 A:Residues: 1-185 <HUD>
 A:CROSS-references: GB:X00948; NID:935926; PIDN:CAA25460.1; PID:935927
 R:Stults, J.F.; Bourell, J.H.; Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow, R.
 Biomed. Environ. Mass Spectrom. 19, 655-664, 1990

A;Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaeoptera acut
A;Reference number: A32201; MUID:89093167
A;Accession: B32201
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-54 <SCH>
C;Superfamily: Insulin

Query Match 40.7%; Score 61; DB 2; Length 54;
Best Local Similarity 42.9%; Pred. No. 0.039;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGSRW 27
:: ||||| :| :| || ||
Db 7 IKACGRELVLRLWVEICGSVRW 27

RESULT 13
S48082
relaxin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C;Accession: S48082; PC2067; PN0626
R;Evans, B.A.; John, M.; Fowler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear,
J. Mol. Endocrinol. 10, 15-23, 1993
A;Title: The mouse relaxin gene: nucleotide sequence and expression.
A;Reference number: S48082; MUID:93199663
A;Accession: S48082
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-185 <EVA>
A;Cross-references: EMBL:Z27088; NID:G414780; PIDN:CAA81611.1; PID:G414781
R;Buellesbach, E.E.; Schwabe, C.
Biochem. Biophys. Res. Commun. 196, 311-319, 1993
A;Title: Mouse relaxin: synthesis and biological activity of the first relaxin with a
A;Reference number: PN0626; MUID:94030011
A;Accession: PC2067
A;Molecule type: protein
A;Residues: 23-57 <BUE>
A;Accession: PN0626
A;Molecule type: protein
A;Residues: 161-185 <BUZ>
A;Note: proteins with and without 184-Tyr were synthesized, their biological activity
C;Superfamily: Insulin
C;Keywords: hormone
F:23-57/161-185/Product: relaxin #status experimental <MAT>
F:23-57/Domain: chain B #status experimental <CHB>
F:161-185/Domain: chain A #status experimental <CHA>
F:36-171,48-185,170-175/Disulfide bonds: #status experimental

Query Match 40.7%; Score 61; DB 2; Length 185;
Best Local Similarity 52.6%; Pred. No. 0.12;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGS 25
:||||| :| :| || |
Db 33 IRMCGREYARELIKTCGAS 51

RESULT 14
A53879
relaxin - dog (fragments)
C;Species: Canis lupus familiaris (dog)
C;Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: B53879; A53879
R;Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A;Title: Purification and sequence determination of canine relaxin.
A;Reference number: A53879; MUID:93000391
A;Accession: B53879
A;Molecule type: protein

A;Residues: 1-35 <STE>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115401)
 A;Accession: A53879
 A;Molecule type: protein
 A;Residues: 36-59 <ST2>
 A;Experimental source: placenta
 A;Note: sequence extracted from NCBI backbone (NCBIP:115399)
 C;Superfamily: insulin
 C;Keywords: hormone
 F:1-35/36-59/Product: relaxin #status experimental <MAT>
 F:1-35/Domain: chain B #status experimental <CHB>
 F:36-59/Domain: chain A #status experimental <CHA>
 F:9-46,21-59,45-50/Disulfide bonds: #status predicted

Query Match 40.0%; Score 60; DB 2; Length 59;
 Best Local Similarity 42.9%; Pred. No. 0.06;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

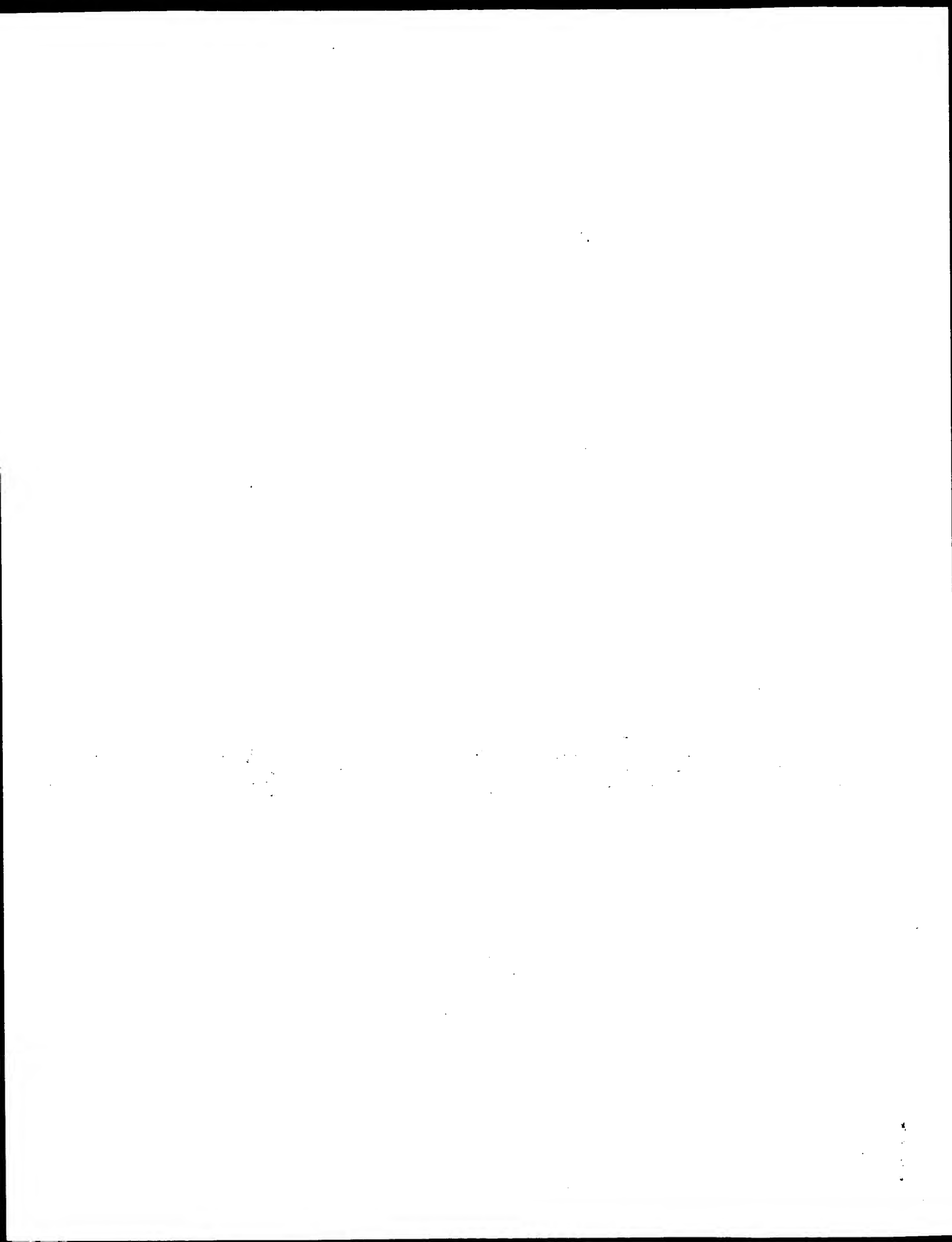
QY 7 VRLCGREFIRAVIFTCGGSRW 27
 :: |||:::| | || |
 Db 6 LKACGRDVRVRLQIEVCGSSW 26

RESULT 15
 I56451
 relaxin - hamadryas baboon (fragment)
 C;Species: Papio hamadryas (hamadryas baboon)
 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 01-Dec-2000
 C;Accession: I56451; S42782
 R;Evans, B.B.A.; Fu, P.; Tregear, G.G.W.
 J. Mol. Endocrinol. 140, 385-392, 1994
 A;Title: Characterization of two relaxin genes in the chimpanzee.
 A;Reference number: I56451
 A;Accession: I56451
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-33 <EVA>
 A;Cross-references: EMBL:Z27224; NID:g415994; PIDN:CAAB1738.1; PID:g415995
 A;Note: submitted to the EMBL Data Library, November 1993
 C;Genetics:
 A;Gene: rlx
 C;Superfamily: insulin
 C;Keywords: hormone
 F:1-33/Domain: relaxin chain B (fragment) #status predicted <RXB>

Query Match 38.0%; Score 57; DB 2; Length 33;
 Best Local Similarity 52.6%; Pred. No. 0.1;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVIFTCGGS 25
 :: |||| :|| | || |
 Db 8 IKACGRELVRQIAICGKS 26

Search completed: June 27, 2002, 16:09:27
 Job time: 211 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 16:16:51 ; Search time 18.68 Seconds
(without alignments)
55.965 Million cell updates

Title: US-09-781-077-2_COPY_26_52
Perfect score: 150
Sequence: 1 RAAPYGVRLCGREFIRAVIFTCGG

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database : SwissProt 40:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query No. | Score | % | | DB | ID | Description |
|------------|-----------|-------|-------|--------|----|-------------|---------------------|
| | | | Match | Length | | | |
| 1 | 1 | 116 | 77.3 | 54 | 1 | RELX_SQUAC | P11953 squalus aca |
| 2 | 2 | 96 | 64.0 | 44 | 1 | RELX_ODOTFA | P01349 odontaspis |
| 3 | 3 | 87 | 58.0 | 64 | 1 | RELX_RAJER | P11952 raja erinac |
| 4 | 4 | 82 | 54.7 | 135 | 1 | INL5_HUMAN | Q9Y5q6 homo sapien |
| 5 | 5 | 76 | 50.7 | 131 | 1 | INL3_HUMAN | P51460 homo sapien |
| 6 | 6 | 75 | 50.0 | 131 | 1 | INL3_PIG | P51461 sus scrofa |
| 7 | 7 | 75 | 50.0 | 132 | 1 | INL3_BOVIN | O77801 bos taurus |
| 8 | 8 | 75 | 50.0 | 135 | 1 | INL5_MOUSE | Q9Wug6 mus musculu |
| 9 | 9 | 72 | 48.0 | 166 | 1 | REL2_PANTR | P51455 pan troglod |
| 10 | 10 | 71 | 47.3 | 166 | 1 | REL1_PANTR | P51454 pan troglod |
| 11 | 11 | 71 | 47.3 | 185 | 1 | REL1_HUMAN | P04808 homo sapien |
| 12 | 12 | 71 | 47.3 | 185 | 1 | REL2_HUMAN | P04090 homo sapien |
| 13 | 13 | 70 | 46.7 | 105 | 1 | INL3_RAT | Q9Wuk0 rattus norv |
| 14 | 14 | 69 | 46.0 | 131 | 1 | INL3_CALJA | O97937 callithrix |
| 15 | 15 | 66 | 44.0 | 122 | 1 | INL3_MOUSE | O09107 mus musculu |
| 16 | 16 | 61 | 40.7 | 54 | 1 | RELX_BALAC | P11184 balaeonopter |
| 17 | 17 | 61 | 40.7 | 185 | 1 | RELX_MOUSE | P47932 mus musculu |
| 18 | 18 | 57 | 38.0 | 185 | 1 | RELX_MACNU | P19884 macaca mula |
| 19 | 19 | 55 | 36.7 | 54 | 1 | RELX_BALED | P11185 balaeonopter |
| 20 | 20 | 55 | 36.7 | 177 | 1 | RELX_MESAU | O64171 mesocricetu |
| 21 | 21 | 55 | 36.7 | 182 | 1 | RELX_PIG | P01348 sus scrofa |
| 22 | 22 | 54 | 36.0 | 177 | 1 | RELX_CANFA | Q9Ytrm8 canis fami |
| 23 | 23 | 54 | 36.0 | 191 | 1 | INL6_MOUSE | Q9YqW05 mus musculu |
| 24 | 24 | 53 | 35.3 | 106 | 1 | ILB2_CABEL | Q09627 caenorhabdi |
| 25 | 25 | 53 | 35.3 | 188 | 1 | INL6_RAT | Q9Wv41 rattus norv |
| 26 | 26 | 52 | 34.7 | 182 | 1 | RELX_HORSE | P22969 equus cabal |
| 27 | 27 | 51 | 34.0 | 112 | 1 | ILB5_CABEL | P56174 caenorhabdi |
| 28 | 28 | 51 | 34.0 | 186 | 1 | RELX_RAT | P01347 rattus norv |
| 29 | 29 | 51 | 34.0 | 886 | 1 | SUHW_DROAN | Q08875 drosophila |
| 30 | 30 | 50 | 33.3 | 448 | 1 | ZFG1_CHICK | Q92010 gallus gall |
| 31 | 31 | 50 | 33.3 | 449 | 1 | ZFG1_HUMAN | O43629 homo sapien |
| 32 | 32 | 50 | 33.3 | 449 | 1 | ZFG1_MOUSE | Q08376 mus musculu |
| 33 | 33 | 49.5 | 33.0 | 106 | 1 | ILB1_CABEL | O09626 caenorhabdi |

| | | | | | | | |
|----|----|------|-----|---|------------|--------|-------------|
| 34 | 49 | 32.7 | 59 | 1 | INS_HYDGO | P09536 | hydrolagus |
| 35 | 49 | 32.7 | 89 | 1 | INS_CALMI | P13190 | callorhynch |
| 36 | 49 | 32.7 | 107 | 1 | ILB3_CABEL | Q03628 | caenorhabdi |
| 37 | 49 | 32.7 | 81 | 1 | INL6_HUMAN | Q95781 | homo sapien |
| 38 | 48 | 32.0 | 213 | 1 | RELX_DASSA | P81191 | dasyatis sa |
| 39 | 48 | 32.0 | 160 | 1 | RELX_CAVPO | P51453 | cavia porce |
| 40 | 48 | 32.0 | 201 | 1 | 2F39_MOUSE | Q02525 | mus musculu |
| 41 | 48 | 32.0 | 594 | 1 | NU5M_HIPAM | Q92571 | hippopotamu |
| 42 | 48 | 32.0 | 598 | 1 | NU5M_PETMA | Q35543 | petromyzon |
| 43 | 48 | 32.0 | 601 | 1 | NU5M_DASNO | Q21335 | gasypus nov |
| 44 | 48 | 32.0 | 602 | 1 | NU5M_DIDMA | P41309 | didelphis m |
| 45 | 48 | 32.0 | 602 | 1 | NU5M_MACRO | P92669 | macropus ro |

ALIGNMENTS

| | |
|------------------|----------------------------------------------------------------------|
| RESULT | 1 |
| ID RELX_SQUAC | STANDARD; PRT; 54 AA. |
| AC | P11953; |
| DT | 01-OCT-1989 (Rel. 12, Created) |
| DT | 01-FEB-1994 (Rel. 28, Last sequence update) |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) |
| DE | Relaxin. |
| OS | Squalus acanthias (Spiny dogfish). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; |
| OX | Elasmobranchii; Squales; Squaloidei; Squalidae; Squalus. |
| NCBI_TaxID=7797; | |
| [1] | SEQUENCE. |
| RN | TISSE-Ovary; |
| RP | MEDLINE=87054035; PubMed=3780747; |
| RA | Bullerbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E., |
| CA | Callard I.P.; |
| RT | "Isolation, purification, and the sequence of relaxin from spiny |
| RT | dogfish (<i>Squalus acanthias</i>)."; |
| RL | Eur. J. Biochem. 161:335-341(1986). |
| CC | -I- FUNCTION: THE FUNCTION OF RELAXIN IN AN OVIPAROUS SPECIES IS NOT |
| CC | YET KNOWN. |
| CC | -I- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO |
| CC | DISULFIDE BONDS. |
| CC | -I- SUBCELLULAR LOCATION: Secreted. |
| CC | -I- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. |
| PIR | A26463; A26463. |
| PIR | B26463; B26463. |
| DR | HSSP; P04090; 6RLX. |
| DR | InterPro: IPR000739; Insulin_IGF_relaxin. |
| DR | Pfam: PF00049; Insulin; 1. |
| DR | SMART: SM00078; ILGF; 1. |
| DR | PROSITE: PS00262; INSULIN; 1. |
| KW | Insulin family; Hormone. |
| CHAIN | 1 30 RELAXIN B CHAIN. |
| FT | NON_CONS 30 31 |
| FT | CHAIN 31 54 RELAXIN A CHAIN. |
| FT | MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID. |
| FT | DISULFD 13 41 INTERCHAIN. |
| FT | DISULFD 25 54 INTERCHAIN. |
| FT | DISULFD 40 45 |
| SQ | SEQUENCE 54 AA; 5910 MW; 1B7206773AD32A5B CRC64: |

```
Query Match          77.3%; Score 116; DB 1; Length 54;
Best Local Similarity 86.4%; Pred. NO. 6.3e-11;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

| QY | 6 | GVR | LC | GR | EF | IR | AV | IF | TC | GS | SR | 27 |
|----|---|-----|----|----|----|----|----|----|----|----|----|----|
| | | | : | : | | | | | | | | |
| Db | 9 | G | I | K | L | C | G | R | E | F | I | R |
| | | A | V | I | Y | T | C | G | S | R | W | 30 |

RESULT 2
RELX ODOTA


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DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 48 INSULIN-LIKE PEPTIDE INSLS B CHAIN
FT PROPEP 49 114 (POTENTIAL).
FT CHAIN 115 135 CONNECTING PEPTIDE (POTENTIAL).
FT DISULFID 29 122 INSULIN-LIKE PEPTIDE INSLS A CHAIN
FT DISULFID 41 135 (POTENTIAL).
FT DISULFID 121 126 INTERCHAIN (BY SIMILARITY).
FT DISULFID 121 126 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 135 AA; 15318 MW; 98FFCB20E9C4BC1F CRC64;

Query Match 54.7%; Score 82; DB 1; Length 135;
Best Local Similarity 66.7%; Pred No. 1.9e-05;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 VRLCGREFTRAVITFCGSRW 27
Db 26 VRLCGLEYIRTVIYCASSRW 46
||||| I:|:| I:| I:|

RESULT 5
INL3_HUMAN STANDARD; PRT; 131 AA.
AC P51460; Q9UEA2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
GN INSL3 OR RLF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Burkhardt E., Adham I.M., Hobohm U., Murphy D., Sander C., Engel W.;
RT "A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).";
RL Hum. Genet. 94:91-94(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292172; PubMed=8020942;
RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
RA Engel W.;
RT "Structural organization of the porcine and human genes coding for a
RT Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
RT localization of the human gene (INSL3).";
RL Genomics 20:13-19(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Vliswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan P., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~700 kb region in 19p13.1 between JAK3 and
RT PDE4C.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC -!- SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC -!- DISULFIDE BONDS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND
CC POSTNATAL LEYDIG CELLS. FOUND AS WELL IN THE CORPUS LUTEUM,
CC TROPHOBLAST, FETAL MEMBRANES AND BREAST.

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CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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CC -----
DR EMBL; S72482; AAB31371.1;
DR EMBL; X73637; CAA52017.1; ALT_SEQ.
DR EMBL; AC005952; AAC72277.1;
DR MIM; 146738;
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 55 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
FT PROPEP 58 104 C PEPTIDE (POTENTIAL).
FT CHAIN 106 131 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
FT DISULFID 34 116 INTERCHAIN (BY SIMILARITY).
FT DISULFID 46 129 INTERCHAIN (BY SIMILARITY).
FT DISULFID 115 120 BY SIMILARITY.
FT CONFLICT 60 60 A -> T (IN REF. 3).
SQ SEQUENCE 131 AA; 14472 MW; C5799D610424C136 CRC64;

Query Match 50.7%; Score 76; DB 1; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00015;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFTRAVITFCGSRW 27
Db 32 KLCGHFVRALVRCGGPRW 51
||||| I:|:| I:| I:|

RESULT 6
INL3_PIG STANDARD; PRT; 131 AA.
AC P51461;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
GN INSL3 OR RLF.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94075362; PubMed=8253799;
RA Adham I.M., Burkhardt E., Benahmed M., Engel W.;
RT "Cloning of a cDNA for a novel insulin-like peptide of the testicular
RT Leydig cells.";
RL J. Biol. Chem. 268:26668-26672(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292172; PubMed=8020942;
RA Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
RA Engel W.;
RT "Structural organization of the porcine and human genes coding for a
RT Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal
RT localization of the human gene (INSL3).";
RL Genomics 20:13-19(1994).
CC -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
CC -!- SPERMATOGENESIS.
CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC -!- DISULFIDE BONDS (BY SIMILARITY).

```


CC DISULFIDE BONDS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
CC BUT NOT IN THE PLACENTA.
CC -|- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 227225; CAA81739.1; -
DR HSP; P04090; 6RLX.
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 5 POTENTIAL.
FT CHAIN 6 34 RELAXIN B CHAIN (PROBABLE).
FT PROPEP 37 139 CONNECTING PEPTIDE (PROBABLE).
FT CHAIN 143 166 RELAXIN A CHAIN (PROBABLE).
FT DISULFID 16 153 INTERCHAIN (BY SIMILARITY).
FT DISULFID 28 166 INTERCHAIN (BY SIMILARITY).
FT DISULFID 152 157 BY SIMILARITY.
SO SEQUENCE 166 AA; 18730 MW; 7F469B1F9259F4F CRC64;

Query Match 47.3%; Score 71; DB 1; Length 166;
Best Local Similarity 57.1%; Pred. No. 0.0011;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 7 VRLCGREFIRAVIFTCGSRW 27
Db 13 IKLCGRELVRQIAICGMSTW 33

RESULT 11
ID RELI_HUMAN STANDARD; PRT; 185 AA.
AC P04808; Q99936;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prorelaxin H1 precursor.
GN RLNI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=85051298; PubMed=6548702;
RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
RA Gorman J., Tregear G., Shine J., Niall H.;
RT "Relaxin gene expression in human ovaries and the predicted structure
RT of a human prorelaxin by analysis of cDNA clones.";
RL EMBO J. 3:2333-2339(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=83141755; PubMed=6298628;
RA Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
RA Tregear G., Shine J., Niall H.;
RT "Structure of a genomic clone encoding biologically active human
RT relaxin.";
RL Nature 301:628-631(1983).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Sehra H.;

Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Prostate;
RA Strausberg R.;
[5]
RN PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnerson J.W., Fu P., Roche P.J., Tregear G.W.;
RT "Expression of human relaxin genes: Characterization of a novel
RT alternatively-spliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
CC -|- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
CC PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
CC INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY.
CC PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
CC -|- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -|- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
CC or ovary.
CC -|- MISCELLANEOUS: H1 RELAXIN MAY BE A PSEUDOGENE.
CC -|- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00949; CAA25461.1; -
DR EMBL; V00578; CAA23839.1; -
DR EMBL; V00577; CAA23838.1; -
DR EMBL; A06926; CAA00603.1; -
DR EMBL; A06846; CAA00599.1; -
DR EMBL; A07364; CAA00658.1; -
DR EMBL; A07329; CAA01325.1; -
DR EMBL; AL135786; CAC04179.1; -
DR EMBL; BC005956; AAH05956.1; -
DR EMBL; S83200; AAD14429.1; -
DR PIR; A44559; A44559.
DR HSP; P04090; 6RLX.
DR MIM; 179730; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00276; INSULINA.
DR SMART; SM00078; ILGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Insulin family; Hormone; Multigene family; Signal;
FT SIGNAL 1 22 PROBABLE.
FT CHAIN 23 53 RELAXIN B CHAIN (PROBABLE).
FT PROPEP 56 158 CONNECTING PEPTIDE (PROBABLE).
FT CHAIN 163 185 RELAXIN A CHAIN (PROBABLE).
FT DISULFID 35 172 INTERCHAIN (BY SIMILARITY).
FT DISULFID 47 185 INTERCHAIN (BY SIMILARITY).
FT DISULFID 171 176 BY SIMILARITY.
FT VARSPLIC 71 117 EIVPSFNKDTETIIIMLEFANLPPELKAALSERQPSLPE
FT LQQYVP -> GDFIOTVSGIDPGKALRTGSCFTREFLG
FT ALSKLYHPSSTKIOKL (IN ISOFORM 2).
FT MISSING (IN ISOFORM 2).
FT K -> M (IN DBSNP:618066).
FT /FTIQ=VAR_011962.
FT SEQUENCE 185 AA; 21145 MW; B318628ABFEC7142 CRC64;

Query Match 47.3%; Score 71; DB 1; Length 185;
Best Local Similarity 57.1%; Pred. No. 0.0012; 6; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
Db 32 IKLCGRELVAQIAICGMSTW 52

RESULT 12
REL2_HUMAN STANDARD; PRT; 185 AA.
AC P04030; Q9UCX3; Q99936;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Prorolaxin H2 precursor.
GN RLN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=85051298; PubMed=6548702;
RA Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
RA Gorman J., Tregear G., Shine J., Niall H.;
RT "Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones.";
RL EMBO J. 3:2333-2339(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Sehra H.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnarsen J.M., Fu P., Roche P.J., Tregear G.W.;
RT "Expression of human relaxin genes: characterization of a novel
alternatively-spliced human relaxin mRNA species.";
RL Mol. Cell. Endocrinol. 118:85-94(1996).
RN [4]
RP SYNTHESIS.
RX MEDLINE=91250367; PubMed=2040595;
RA Buellbach E.E., Schwabe C.;
RT "Total synthesis of human relaxin and human relaxin derivatives by
solid-phase peptide synthesis and site-directed chain combination.";
RL J. Biol. Chem. 266:10734-10761(1991).
RN [5]
RP PARTIAL SEQUENCE OF 25-51.
RC TISSUE=Semen;
RX MEDLINE=92241162; PubMed=1572287;
RA Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T.,
RA Goldsmith L.T.,
RT "Human seminal relaxin is a product of the same gene as human luteal
relaxin.";
RL Endocrinology 130:2660-2668(1992).
RN [6]
RP SEQUENCE OF 25-53 AND 162-185.
RX MEDLINE=91167739; PubMed=2076464;
RA Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.;
RT "Structural characterization by mass spectrometry of native and
recombinant human relaxin.";
RL Biomed. Environ. Mass Spectrom. 19:655-664(1990).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=92015205; PubMed=1656049;
RA Eigenbrot C., Randal M., Quan C., Burnier J., O'Connell L.,
RA Rinderknecht E., Kossiakoff A.A.;
RT "X-ray structure of human relaxin at 1.5 A. Comparison to insulin and
implications for receptor binding determinants.";

J. Mol. Biol. 221:15-21(1991).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
PRODUCE DILATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY.
PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also
expressed in placenta, decidua and prostate.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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EMBL; X00948; CAA25460.1; -
EMBL; AL135786; CAC04177.1; -
EMBL; AL135786; CAC04176.1; -
EMBL; S83200; AAD14429.1; -
EMBL; A17315; CAA01324.1; -
EMBL; A05925; CAA00602.1; -
PIR; A60982; A60982.
PDB; 6RLX; 31-OCT-93.
MIM; 179740; -
InterPro: IPR000739; Insulin_IGF_relxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal; 3D-structure;
Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 53 RELAXIN B CHAIN.
FT PROPEP 56 157 CONNECTING PEPTIDE.
FT CHAIN 162 185 RELAXIN A CHAIN.
FT MOD_RES 162 162 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 35 172 INTERCHAIN.
FT DISULFID 47 185 INTERCHAIN.
FT DISULFID 171 176
FT VARSPLIC 71 117
FT FT
FT FT
FT VARSPLIC 118 185
FT HELIX 27 29
FT STRAND 31 32
FT HELIX 36 49
FT HELIX 163 173
FT TURN 174 174
FT STRAND 176 177
FT HELIX 178 182
FT TURN 183 184
SQ SEQUENCE 185 AA; 21042 MW; AC73DBDE2090091B CRC64;
Query Match 47.3%; Score 71; DB 1; Length 185;
Best Local Similarity 57.1%; Pred. No. 0.0012; 6; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
Db 32 IKLCGRELVAQIAICGMSTW 52

RESULT 13
INL3_RAT
ID INL3_RAT
AC Q9WUK0;

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.
TISSUE=Testis;
MEDLINE=96366811; PubMed=8770925;
Rusch W., Balvers M., Ivell R.;
"Molecular cloning and expression of the relaxin-like factor from the
mouse testis";
Endocrinology 137:3009-3013(1996).
[3]

SEQUENCE FROM N.A.
STRAIN=129/SVJ;
MEDLINE=98088907; PubMed=9428631;
Koskimies P., Spiess A.N., Lahti P., Huhtaniemi I., Ivell R.;
"The mouse relaxin-like factor gene and its promoter are located
within the 3' region of the JAK3 genomic sequence.";
FEBS Lett. 419:186-190(1997).

-1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
SPERMATOGENESIS.
-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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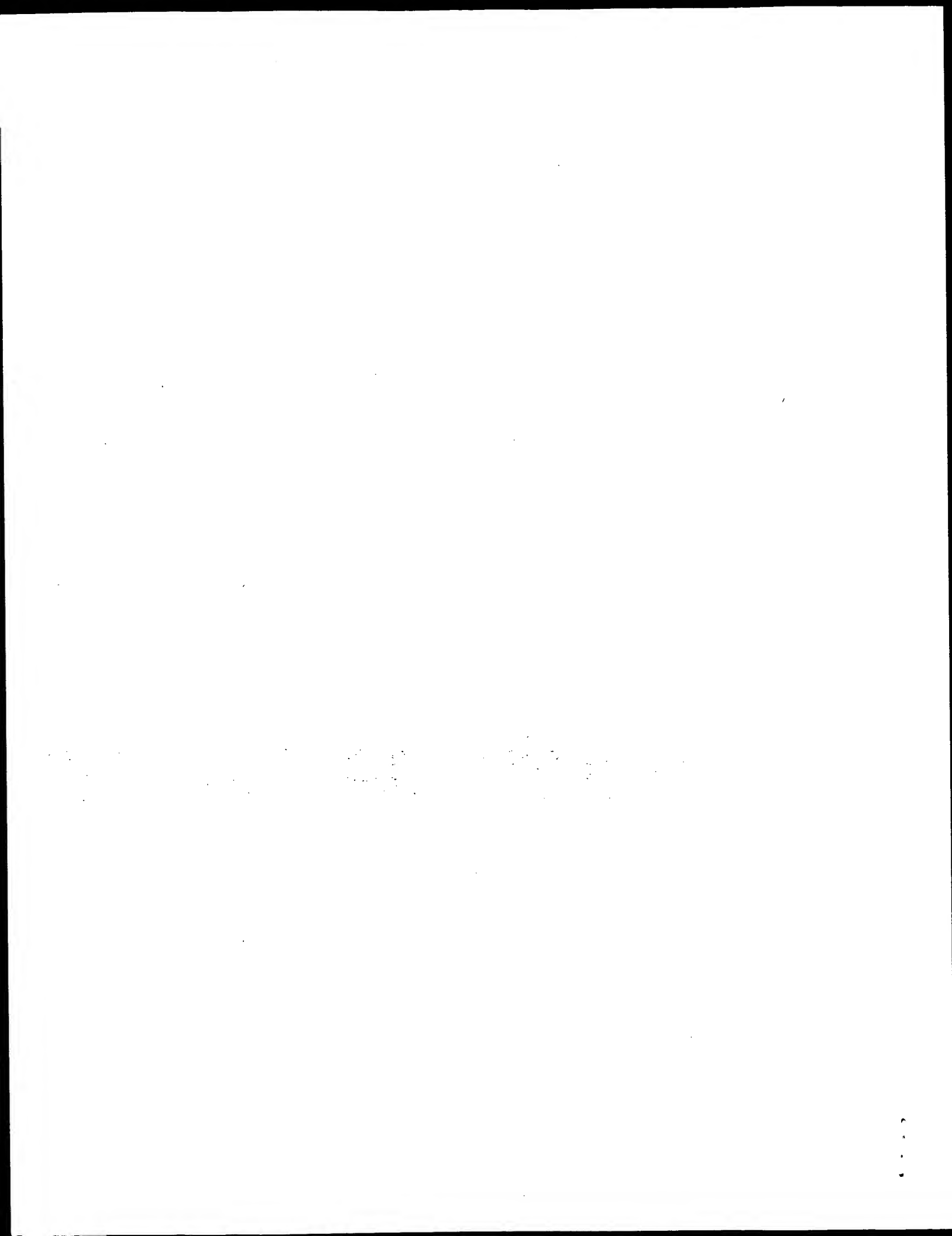
EMBL; X95603; CAA64861.1; -
EMBL; S82815; AAB39365.1; -
EMBL; AF136524; AAD24585.1; -
MGD; MGI:108427; Insl3.
InterPro: IPR000739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
SIGNAL 1 15
CHAIN 16 ?
FT CHAIN 16 ?
FT PROPEP ? 94
FT CHAIN 97 122
FT DISULFID 29 107
FT DISULFID 41 120
FT DISULFID 106 111
FT CONFLICT 21 21
FT CONFLICT 54 58
FT CONFLICT 73 73
FT CONFLICT 92 96
FT SEQUENCE 122 AA; 13586 MW; 10783AB4896CF103 CRC64;

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Query Match      44.0%; Score 66; DB 1; Length 122;
Best Local Similarity 45.0%; Pred. NO. 0.0044;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Search completed: June 27, 2002, 16:16:52
Job time: 486 sec




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RESULT 2
Q9UPH6 PRELIMINARY: PRT; 65 AA.
ID Q9UPH6
AC Q9UPH6
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INL3_HUMAN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Scott D.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Sakalidis G., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,
RA Erler A., Christensen M., Georgescu A., Avila J., Attix C.,
RA Andreise T., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C.,
RA Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.,
RA "Sequence analysis of a 5.7 Mb region in 19p13.1."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007201; AAD22740.1; -
FT NON_TER 65
SQ SEQUENCE 65 AA; 7088 MW; 9D0BF767161DE030 CRC64;

Query Match 50.7%; Score 76; DB 4; Length 65;
Best Local Similarity 55.0%; Pred. No. 0.00026;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
Db 32 KLCGHHFVRALVRCGPRW 51
:|||||:|||||
:|||||:|||||

RESULT 3
Q9NOT8 PRELIMINARY: PRT; 131 AA.
ID Q9NOT8
AC Q9NOT8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoides;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20150568; PubMed=10687860;
RA Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
RA Fischer B., Klonisch I.;
RA "Relaxin-like factor (RLF) mRNA expression in the fallow deer.";
RL Mol. Cell. Endocrinol. 159:147-158(2000).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF254740; AAF67742.1; -
DR EMBL; AF254740; AAF67742.1; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14406 MW; EC7731679E60B0C7 CRC64;

Query Match 50.0%; Score 75; DB 6; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00075;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
Db 32 KLCGHHFVRALVRCGPRW 51
:|||||:|||||
:|||||:|||||

RESULT 4
Q9GK47 PRELIMINARY: PRT; 131 AA.
ID Q9GK47
AC Q9GK47
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN-LIKE PROTEIN.
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
OX NCBI_TaxID=9463;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=TESTIS;
RA Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.;
RA "Molecular remodeling of members of the relaxin family during primate
RA evolution.";
RL Mol. Biol. Evol. 0:0-0(2001).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF317624; AAG42317.1; -
DR InterPro; IPR000739; Insulin_IGF_relaxin.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
SQ SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;

Query Match 50.0%; Score 75; DB 6; Length 131;
Best Local Similarity 55.0%; Pred. No. 0.00075;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
Db 32 KLCGHHFVRALVRCGPRW 51
:|||||:|||||
:|||||:|||||

RESULT 5
Q28431 PRELIMINARY: PRT; 33 AA.
ID Q28431
AC Q28431
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXIN (FRAGMENT).
GN RLX.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Evans B.B.A., Fu P., Tregear G.G.W.;
RA "Characterisation of primate relaxin genes.";
RL J. Mol. Endocrinol. 0:0-0(1993).
DR EMBL; Z27237; CAA81751.1; -
DR HSSP; P04090; 6RLX.
FT NON_TER 1
SQ SEQUENCE 33 AA; 3766 MW; 54BE68D028EDA2F6 CRC64;

Query Match 47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00073;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
Db 8 IKLCGRELVRQAICGMSTW 28
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Query Match 44.7%; Score 67; DB 6; Length 131;
 Best Local Similarity 50.0%; Pred. No. 0.013;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 DB 32 KLCGHHSVRALVRLCGGPRW 51

RESULT 7
 Q28429 ID Q28429 PRELIMINARY; PRT; 33 AA.
 AC Q28429
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RG YK 287;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; 227227; CAA81741.1;
 DR HSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3710 MW; 8AC798A03481D2EF CRC64;

Query Match 44.7%; Score 67; DB 6; Length 131;
 Best Local Similarity 50.0%; Pred. No. 0.013;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 DB 32 KLCGHHSVRALVRLCGGPRW 51

RESULT 7
 Q28429 ID Q28429 PRELIMINARY; PRT; 33 AA.
 AC Q28429
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RG YK 287;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; 227227; CAA81741.1;
 DR HSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3710 MW; 8AC798A03481D2EF CRC64;

Query Match 44.7%; Score 67; DB 6; Length 131;
 Best Local Similarity 50.0%; Pred. No. 0.013;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 DB 32 KLCGHHSVRALVRLCGGPRW 51

RESULT 7
 Q28429 ID Q28429 PRELIMINARY; PRT; 33 AA.
 AC Q28429
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RG YK 287;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; 227227; CAA81741.1;
 DR HSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3710 MW; 8AC798A03481D2EF CRC64;

Query Match 44.7%; Score 67; DB 6; Length 131;
 Best Local Similarity 50.0%; Pred. No. 0.013;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLCGREFIRAVFTCGGSRW 27
 DB 32 KLCGHHSVRALVRLCGGPRW 51

RESULT 7
 Q28429 ID Q28429 PRELIMINARY; PRT; 33 AA.
 AC Q28429
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RG YK 287;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; 227227; CAA81741.1;
 DR HSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3710 MW; 8AC798A03481D2EF CRC64;

Query Match 42.0%; Score 63; DB 6; Length 33;
 Best Local Similarity 52.4%; Pred. No. 0.012;
 Matches 11; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 7 VRLCGREFIRAVFTCGGSRW 27
 DB 8 IKLCGCELVRAQIAICGMSTW 28

RESULT 8
 Q9N0F2 ID Q9N0F2 PRELIMINARY; PRT; 73 AA.
 AC Q9N0F2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE LEYDIG CELL-SPECIFIC INSULIN-LIKE PEPTIDE (FRAGMENT).
 GN INSL3.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=THOROUGHRED; TISSUE=TESTIS;
 RA Hasegawa T.;
 RT "Nucleotide sequence of equine Leydig cell-specific insulin-like peptide."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033169; BAA97580.1;
 FT NON_TER 1
 FT NON_TER 73
 SQ SEQUENCE 73 AA; 8125 MW; B9DCBA6D0D72C8BD CRC64;

Query Match 40.7%; Score 61; DB 6; Length 73;
 Best Local Similarity 52.9%; Pred. No. 0.056;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 11 GREFIRAVFTCGGSRW 27
 DB 1 GHFVRLVRCVCGPRW 17

RESULT 9
 Q9MYK8 ID Q9MYK8 PRELIMINARY; PRT; 180 AA.
 AC Q9MYK8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RELAXIN.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99115216; PubMed=9915995;
 RA Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
 RA Steger K., Huppertz B., Fischer B.;
 RT "Nucleic acid sequence of feline preprorelaxin and its localization within the feline placenta."
 RL Biol. Reprod. 60:305-311(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hombach-Klonisch S., Klonisch T.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF233688; AAF60303.1;
 DR HSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 180 AA; 19000739; Insulin_IGF_relaxin.

DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN: 1.
 SQ SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;

Query Match 40.7%; Score 61; DB 6; Length 180;
 Best Local Similarity 47.6%; Pred. No. 0.14;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 :: ||||| : || |
 Db 30 LKACGREFVRLQIRICGSLW 50

RESULT 10
 Q28788 PRELIMINARY; PRT; 33 AA.
 ID Q28788
 AC Q28788;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BABA;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterization of two relaxin genes in the chimpanzee."
 RL J. Mol. Endocrinol. 140:385-392(1994).
 DR EMBL; 227224; CAA81738.1; -.
 DR HSSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3618 MW; DD8498A0353F9281 CRC64;

Query Match 38.0%; Score 57; DB 6; Length 33;
 Best Local Similarity 52.6%; Pred. No. 0.1;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGS 25
 :: ||||| : || |
 Db 8 IKACGRELVRQIAICGKS 26

RESULT 11
 Q9NOT9 PRELIMINARY; PRT; 199 AA.
 ID Q9NOT9
 AC Q9NOT9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PREPRORELAXIN.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20191540; PubMed=10727251;
 RX Hombach-Klonisch S., Abd-Elmalek M., Skidmore J.A., Leiser R.,
 RA Fischer B., Klonisch T.;
 RT "Ruminant relaxin in the pregnant one-humped camel."
 RL Biol. Reprod. 62:839-846(2000).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 DR EMBL; AF254739; AAF67741.1; -.
 DR HSSP; P01348; 1RLX.
 FT InterPro; IPR000739; Insulin_IGF_relaxin.

DR SMART: SM00078; ILGF: 1.
 DR PROSITE: PS00262; INSULIN: 1.
 SQ SEQUENCE 199 AA; 22386 MW; F69BBD7E4FA8089 CRC64;

Query Match 38.0%; Score 57; DB 6; Length 199;
 Best Local Similarity 47.6%; Pred. No. 0.65;
 Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGGSRW 27
 :: ||||| : || |
 Db 32 VRACGRELVRWLWIEICGSVSW 52

RESULT 12
 Q9TRG5 PRELIMINARY; PRT; 29 AA.
 ID Q9TRG5
 AC Q9TRG5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RELAXIN R-III B CHAIN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93257096; PubMed=8489740;
 RA Kohsaka T., Takahara H., Sugawara K., Tagami S.;
 RT "Endogenous heterogeneity of relaxin and sequence of the major form in pregnant sow ovaries."
 RL Biol. Chem. Hoppe-Seyler 374:203-210(1993).
 DR HSSP; P01348; 1RLX.
 SQ SEQUENCE 29 AA; 3293 MW; 661A9F5DDDESDB10 CRC64;

Query Match 36.7%; Score 55; DB 6; Length 29;
 Best Local Similarity 38.1%; Pred. No. 0.18;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 7 VRLCGREFIRAVIFTCGSRW 27
 :: ||||| : || |
 Db 7 IKACGRELVRWLWIEICGSVSW 27

RESULT 13
 Q28782 PRELIMINARY; PRT; 33 AA.
 ID Q28782
 AC Q28782;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RELAXIN (FRAGMENT).
 GN RLX.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DO PA;
 RA Evans B.B.A., Fu P., Tregear G.G.W.;
 RT "Characterisation of primate relaxin genes."
 RL J. Mol. Endocrinol. 0:0-0(1993).
 DR EMBL; Z27230; CAA81744.1; -.
 DR HSSP; P04090; 6RLX.
 FT NON_TER 1
 SQ SEQUENCE 33 AA; 3752 MW; 225468D127FE9292 CRC64;

Query Match 36.0%; Score 54; DB 6; Length 33;
 Best Local Similarity 47.4%; Pred. No. 0.29;

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